

Fig. 1A

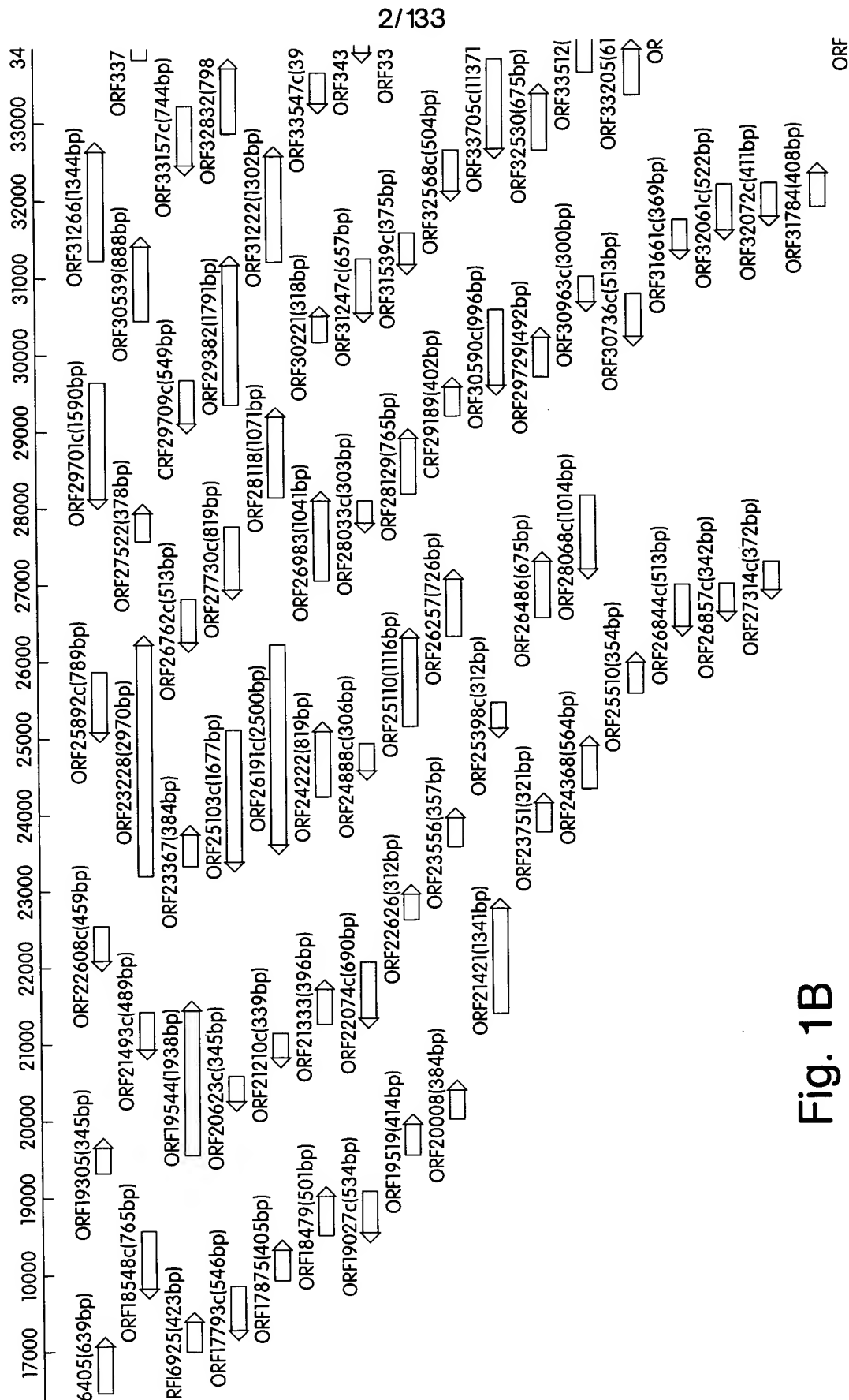


Fig. 1B

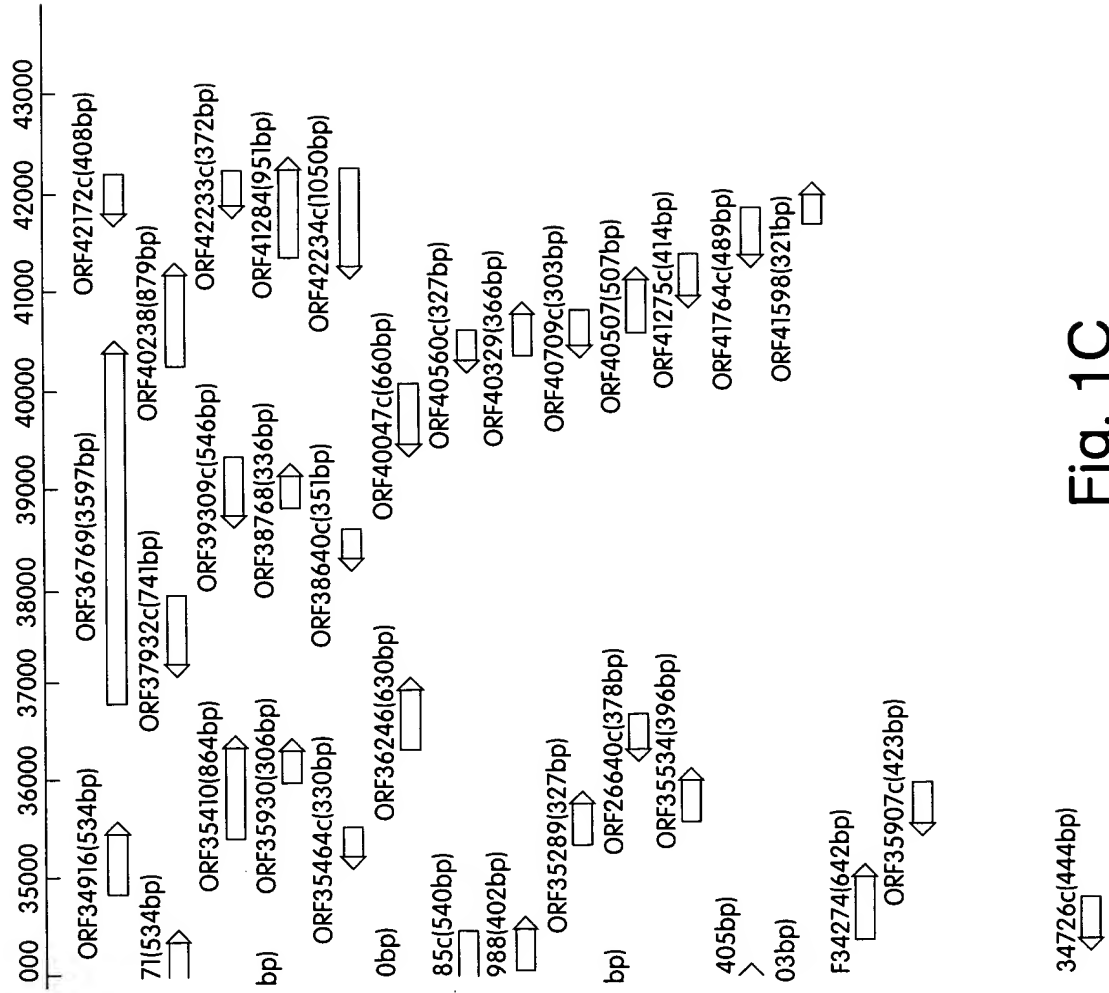


Fig. 1C

BI48 SEQ ID NO:1

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 GGCCCTCAACAGCATCCTCTCCGGCGGCGTCAGCGACATCCGGCAGTGGATGAACAAGTTGTACGGGGAGGCCTTCGCCG
 CCGTCTACGTGCAGCCAGGTGCGCGGGTCGAGTGCATCTCGATCAGCAACTGGCGATCGACTATGAACTCAAGGGCCGC
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 TACACCACCGTGTTCCCTTCTACCAGCGAGTCCAGTACGCCATGCCGGGCGAACGCACGGAGGACTATTGATGGGCTTT
 TTTCAAACCTTCTGCGCGGTGCGACACAGCCTCAGTCGGTACCGGCAGACGCTCCCGAAGATTGAGGAGCGCTGGACGT
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 CGGAGGCAAGCGTGAGACTCTTGAAGGGCGGCTGGGCAGCCAAACGATTTCAAGGTCCCGCCCTGCCCTGGGCGGGGCTG

Fig. 2A

CTGCTGGTCTTGCTGGCTGCATCCGCCGTAGGGGTAGAGCTTCTGGTGAAGGGCCTGCCAGCCAAACCACAGCCTCTACGG
 CGATGCGAAAGCGCGCTGGACGATCAATGAATACGCCGACCTGGAGTGCCCTTCTGCAAGGTCTACACCCCGCGGCTTA
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 GCGACGCGCAAGGAACTGAGCGCGCATGAGCGGACGCGCATTCGCGCGATCGAGATCCTGGTGTGTTGCTGGTCTGCTC

Fig. 2B

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Fig. 2C

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Fig. 2D

TCCTTCGTAAGGGTGGCTACGCACCGGGCACGCTCGGGGATCGGCTGAAGCTAAAAAATCGCACAAACAGCTTTGTAAAC
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 TCACATCGAAAGCCACGACCAATACGAAAACATGGTTTTTGGTAAGCAATACGGATGGCGAAATTCTGGAGCCAGGCAAA
 ACTTACAAAATCAGGGCCTCAACCGATGAGTCTATCCCAAAAATGTGCAAGCTGAGCGTCGGACGATTTTGAAGTCTCA
 GTACGCACTTGCAGATAATTGCGAATTAACCGCTAAATACATAGAGGCCACGGGGCAGAAGTTGTGCGTGTGCAACCGT
 TCATGTGCGACACACCTCCTGAAAAGGGTGGCCTGCCCTGGTAAACCTGGCATAACCATTTGGTACCTTGGTCAAGAA
 TGATGTTTTTATGCCGCCCTGGGCTTTGACGCCGATTAAGCAAAGCTGTGTTGCTCATCCAATACGTCCTCGCCAGT
 TAAACGACTGTTATGTATATGGGTGCTGCCCTACGTAATACCTTGGCCCTACGCATACGAAGTTAATTCTGAAAGCGTT
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 TTTGGCAGCGTCCATATACCGACCGTGGTATGGCTCAGATGCGCTGGTACTGCATTTACCAAAATAAGTTGTGCTATAT
 CGCTCACGGCCGGTATTTCTATCGTCCAAGGCGACATATTGACGATTTCAAGGGTTACGTACCCGTGCAACCCCGGCTCT
 ACCTGACCGTCATTACAGGTTACCTGCACGAACATCGCGCAAGGGTTCCTTTGGTTTGACCCAGACCAAAATAATCTAA
 CGGTATTTGTATCGATGTTTACTGCAGGTGATGACTTGCTCACCAGGATTTCAGCACCAAAATTTGCTGAATTTCTTTTG
 GTTCCAAAAAAAACGTCGACGGGGCTGGATGCGACCCATATACAATGCTTGCAGAGGCGGGCAAAGATTTGGCTCGTAA
 TATGTATGCCCAATTGAATCTTGAGAGAAAACCTGTCAAATAAAGTTTTTTCATATAGCGCATTGCGCAACAAGATG
 TTCTAGATTTTTGTCAATGACAATCATTTTGGCTTAACTTCGTTTCGGCGATGGCTGAGCGTTTTGTTGTGACTGAGGAGG
 CTGCGACTGGTGTTCAGCACAACCTTGTAATAGACGGCGTACATTATAAGAGAAGACACCAGGGAACCTCCGATTAAAT
 TCAGCGTCCACCCGACCCATATGGTGGGATTGAGCGAAAACCACTTCTTCAATCGCGCGCGCGCGTGTGGGAAGCGTC
 GATATTTCACTGCCACGCTTGATGGGGCTTTGGGTGTGCGTCGATTCTGTGGAGAAAAAATCACAGAGCCAAGCTTCTC
 GCCTTTGGTAAGGCAGACATTTTTGTTGGTGGTGTGAATATCCTGAGCTTGAGCTTGCCATCAAATGCAGGTTGACCT
 TCGCCGAAGCAACCAGCAGCGCGCGTGAGAGAAAAAGACTTCCCGTAGGTAGGACTATGCCGTACCGATTGTGCGGCACC
 TTGATTTCTTCAGCGGCCTCCACCACAACAGAATCGTGACCCCTGATCGTCATACCATCGACAATGCGCCACAGGTTTTT
 GTCGTTGCCAGAATAGTTATCACTCCACCCTTCACCCACGGACAATTTCAGGGGAAAACTCTTCAATTCCTCGTCCCCTG
 CATCAGTGAGTATAAGGCTGTTGCTGGAGTACGATGCCGCGTCAAATCCGTGTGGGATTTGTTGTACGCCCTTTGATC
 TGTAACACACTCATCAGATTTGTCTTCTGCTTGGGCTGCGAGACGCGGCCACCCTGCCATTGTCTTTTATACGGCCG
 ATATCCCGGATACCGCTGAAAGATGACGTGCGCAAAGCGTGACCAATCTGAATTTCAAACGCTCGCTGTGATTGTT
 GGTGAGCGCGAAGCTCATCGGCCCTACATAACCTGGAGGCAGCAGTGAACCTGAACGTTATCCCGCTTCTGAACAGCG
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 GGTTCATGACGAAGCAGTCATCCGGGTCTGCGAGCAGACCTCGCTGGCAGGGGTGCGTCGCGTAGATTCTCGCAAGCT
 TCCACCCCTACTGTGAGCGAGAGAGGCTGCGAGTCTGAGGTCAAATCCAACGCTTCCGGGGTGGTCAACTCAGGT
 GGGCAAGGTGCTTGATTAGTTTTCCATCCCGGACCACTTTCAGGAGCGAGTGCAGTGAATCATCTATTTGCTCG
 GGAAGGGCTCAGTCTATAGCACTGAGCAACCGCTACGTTTACAGGCAAAAAGTCGGAAGTCACTGCTGTTGTGCGCGCATTT
 TGCGTGTCTGCGGGTTTAGTAGCAAGGACAAAACCGTGCGACATGCGCAGCGCACTTTCACTGCACGGACAGCCCATC
 GGCATAGCAAGCCTTCAACCGCACTCTGATTGGGCTCACGTCCGACAAGAGTCGAGCAGCTTTCAGAGATTTTCCACATC
 ACCAAAACTGCCAATGGCAGCTAATGGCCGTTCTCTGCTGTGCTCTTTGGCATGACTGGTCAAGTCGGATGCAACG
 GTGGTCAGCACCATTGCAATTGGGTGGTTCATGTGCGATGCAATTACGAGTTGAGCCTGGCCAGTTCTCCCAAGCAAA
 GCATAAGACCAAGATGGCAGATTGCCAACAAAATACCTTCCCGCTACCGTTGTTTTATCGTTGTTGCCAGCCCTGATC
 TGGCGGAAAAGCCCGCTCCATGAATCGTCATGGAGCCTCCATGTTTCACTCCTTTCTGGATATCCAGGAAGCCGTC
 CCCACCCCAACAACCAAGCTGCCCGAGGGGATTCTCTTCTCTGAGCAGCATGGAAGTCTCGGCACGCCTCGCCG
 CCGGACGCTACTGGAGAACATCTGGCAGCGCGCTCGCTATCCAAGCAGCAATTGAGGAGATCTACCGGCGGCCACTGG
 CCAACTATGCCGAGCTGGTCCAGCAGCTCCCTGCTTCGGAATAATCATCACCATGCCATCCAGGCGGGATGATCGATCAC
 GGCTGGAGATCGTGGCTACGCACTCAAGGTACGGCAGACCTACCTGCTCCCGATCGGCGCAGCGCGGAGTCACAGTC
 AGCCAGGCTGAAGCCTGGTCGGCCCGCGCGGCTATGGCGCCCTGGCTCATGACATAGGCAAGATCGTCGTGACCTGC
 AGGTTGAGCTACAGGACGGCAGCACTGGCACCTTGAACGGACCGATCAACCAGCCATACCGCTTCAAGTACGTGAAG
 TCCCGCAATACAGCTCCACGGCGCTGCCTCAGCACTTCTCATCCCAACTGCTACCGCGCACTGCACTCGATTGGCT
 CAGTCGCTTTCAGAGCTGTGGGCTCAATTGATCTACCTGTTGCTGGGAGTACGAGCAGCGCGGGATCTCGGCGAGA

Fig. 2E

TCATCGTGAAGGCAGACCAGGCCTCAGTTGCACAGGAGCTAGGAGGCAATCCGGATCGAGCTCTGGCTGCACCGAAGCAG
 TCGTGCAGCGGCAGTTGGCAGACGGCCTTCGCTTCTTGGTGAAGGACAAGTTCAAGTTGAATCAACCTAGCGGCCCGTC
 TGATGGATGGCTGACCCAGGACGCACTCTGGCTGGTGAGCAAGCCTGCTGCCGATCAACTGAGAGCTACCTGCTGGCCC
 AGGGTATCGATGGGGTGCCCTCCTCTAACCGCGCGTTCTTCAGCATGCTCCAGGACCAAGCCGTCATCCAGACAAATGCC
 GAGGACAAGGCCATTTGGACGGCCACGGTAGACAACGGTCTGGATGGAGAAACAAGTTCACGCTACTCAAGATTGCTCC
 AGCCTTGATCTGGACAGATGCTGCCGAGCGCCCTCACCTACAGCGGATCACTGGTCTGTAAGATGGAACCGCCTCAA
 CGGAAAAGCCGGAACGACCTGTGAAATTCCTAACGGGCCGGCTGAACAGCAGCAAGCACCAGAAACGAAGATGATGCTC
 CATCAACCTGCGCCGAGCGTTGCGAAACCGGCAACGAGACGCGAGCGATTGCGAAACCTCAACTGATGATCAAGAAGA
 AACAGACGATTTGTATGCATTTCTTGGTAATATCAATTCGCCACTAGAAGAGCTAGACACTAGCCACGACTCGCCGGCTG
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 GCAATTGAAGATGTATTTATGCCTAGCAGAAGTACTGATCTGGGACAGGGATTCTGTTGGTGGATGAAATCTGGCATCGC
 GGCCCGTCGCTTTCATCAACGACACCAAGGCTTTGGTGATACCGTAGACGGGACCGCCATGCTGGTCACGCCAGGAA
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 GGTCTTCTACTTCACCGCATCCGGTTGAATGCGCTGTTGTGCATCCGCAAGCGCGACATCGACTGGGAAAATCAACTGA
 TCCTCATCCGCGCGAGACAGAGAAGACTCAAAAGAGTTCTAGTGCCTAATAACGGAGGGGCTTGTCCTCACCTATCG
 AGGCTCCTGCAAGAGGCCGATAGAGCCGATTCGCCGATGACGACCAAGTTGTTCAACGTCAACCGGTTCTCACCGCACTA
 CAAGAGCAAGGTGATGAACTCCGACCAGGTGCAAGCCATGTACCGGAAGTTGACCGAGAAGGTTGGGGTGCGGATGACCC
 CGCACCGTTTTCCGCGCACACCTGGCCACCGACTTGATGAAGGCACCCGAGCGGAACATTACCTCAGGAAGTGCCTGCTC
 AACCACTCGAATATCCAGACCAGATGAGCTACATCGAGCGCGACTACGATCACATGCGTGCCGTGCTGCATGCTAGAAG
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 GCCTGCAGAATGGTTTCAGGGCCTTAGAAAACAGAAAAGCCCACTAGAAAGGCGGGCTATTCCATATTGACATCACGTCA
 ATGCCGGCCTAATGTTCCGCCCAGACGGCTGTAGACAAGAACCAGCGGTAACACCCCTTCTAGCCTATGCAACTCGCCC
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 GACCAAGTATGAGGTGGTTCGGGGTAGAGGATTGGAACCTCCGACATCCTGCTCCCAAAGCAGGCGCGCTACCGGACTG
 CGCTATACCCGATTGGAATTTGGCTCCGCGACCTGGACTCGAACCAAGGACCCAAATGATTAACAGTCATTTGCTTACC
 GACTGAGCTATCGCGAACGTCCTTTCTTCAACCTGAGCGCTTCCGGTGTGCTGGATTGCGCTCAGAGGCGCGCCA
 TTTTACGGATGCGCGCGGGCATGTCAACCTCTGATCCAAAAGTTTTCTTCTTTTCCACGAGCGACAAAACGGCCCT
 TCCACTGCATGCGGCAGCGCTCTCGCGCTACCGGACGCCCATGAAAAAGCCCCGCGGAAGCGGGGCTTTCCCTGTCCGC
 CCCCAGAGGTCAGGCGAAGACGATCTCGTCCGCTTCCACCTTCGCCGAGATACTGGCACCCGGCGCGAATTTGCCGCG
 CAGGATCAGTTGCCCGAGCGGTTCTCGATCCAGCGCTGGATGGCCCGCTTCAGCGGGCGTGCCCATAGACCGGGTCGA
 AGCCGACGGCAATCAGCTTGTCCAGCGCTCCTGGCTCAGTTCCAGGCTCAGCTCGCGCTCGGCCAGGCGCTTGCGCAGG
 CGACCGAGCTGGATCTCGCGGATGCCGGGATCTGCTCGCGAGCCAGCGGCTCGAACACCACCACTTCGTGATCCGGTT

Fig. 2F

GATGAATTCGGACGGAAGTGGCATTGACCGCTCCATCACTGCGGCACGTTGCGCCTCGCGGTGCGCGGCCAGCTCCT
 GGATCTGCGCCGAACCGAGGTTGGAGGTATCACCACCAGGTGTTGCGGAAGTCCACCGTACGCCCCGTAAGTGTGCGGT
 AGGCGTCCGTCTCGAGCAGCTGGAGGAGAAATGTTGAATACATCCGGATGGGCCCTTCTCCACCTCGTCCAGCAGCACCAC
 CGAGTAGGGCTTGGCGCGGATCGCCTCGGTGAGGTAGCCGCTTCTCGAAGCCGACGTAGCCCGAGGCGCGCGGATCA
 GCGGGGCCACCGAGTGTCTCCATGAACTCGGACATATCTATCCGCACCAGCGCTCTCGGTATCGAAGAGGAACCTCG
 GCCAGCGCCTTGACAACTCGGTCTTGCCCAACCCGGTGGGCGGAGGAAGAGGAACGAGCCGCTCGGCCGGTTCGGATC
 GCGGAGGCGCGCGCGAACGGCGCACGGCGTTGGACACGGCGACTACCGCCTCGTCTGGCCGATCACTCGCCGATGCA
 GCTCCTGCTCCATGCGCAGCAGCTTCTCGCGCTCGCCCTCGAGCATCTTCGACACCGGGATACCGGTCCACTTGGAAACC
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 GCTGCGTTCCAGGTCCGGGATGGTCTGGTACTGGATGCGCGCCATGCTCTCGAGGTGCGCCTTGGCGCGCGCCGCTCCA
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 GCGCGGATATCGAAGCCGACCTGCATCAGCAGGGGCTTGTGCAACCGCTTGTCTGCTGAGCAGGGCGGAAAGCAGGTG
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 AGGGGATAGCAATATGGCTCATGTGCACGCGGATCTGGTGGGTACGCCCGGTCTCCAGCTTACCCGGGTATGGGTGTG
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 CGCATGCCGTCCGATCGGCGCATGATGGTGGCGCGGAGGTGATCAGCCGATCAGATCGCCTCGTAGATGCGGCTG
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 CTTGTCCAGGCGGTGGACGATCCCGCGCGCGGCACATTGGCGATGTCCGGGACATGGTAGAGCAAGGCATTACGAGGG
 TGCCGTCTGATGGCGCGCAGCGGATGGACCACAGGCGCGGCGGCTTGTCAATCACCAGGATGTGCTCGTCTCGTAG
 ACGATTTCCAGCTCGATGTCTGTGCGAGCACTCGCCCTGGGCTTCTGCTCGGCTCCAGGACAGTTGCGCGCGGCT

Fig. 2G

GTGGACGATGTCGCGCGGGCGCAGCACGGCGCCGTCGACGGTCAGGCGACCGTCTTGATCCAGCCGGCCAGACGGGAGC
 GGGAGTGTTCGGGAAAAAGCTGGGCGGCGATCTGGTCGAGACGCTGGCCACCCAGCTCGAACGGCACCTCGGCCGCGCGT
 TGAATCATATCGGACATGAGTAGGAGACGATGCTCAGCGCGGCTTTTGAATCGGCTACGCGCTGTGGTTAAATACGGGG
 TCTTTGTCCAGGGGGTGCCTGGGGCGCCAATCATAACAGACGGTTGAGGCCAAGCCGACCGTCCCAGGGACGCAAGCCG
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 GAGAACCTGAGCGAGAGCCAGCTGTACCAGCAGGCGCAGGACGACCTCAACAACAAGAGCTACAACAGCGCCGTACCAA
 GCTGAAAGCCCTCGAATCGCGCTATCCCTTCGGCCGCTACGCCGAGCAGGCCAGCTCGAGCTGATCTACGCCAACTACA
 AGAACATGGAGCCCGAAGCCGCGCCGCGCCGCGCAACGCTTCATCCGCTGCGATCCGCGACCCCCAACGTGACTAC
 GCCTACTACCTCAAAGGCCTGTCTCCTTCGACCAGGACCGCGGCTGCTGGCGCGCTTCTGCCGCTGGACATGACCAA
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 CGGACGCCAAGGCGCGCATGGTGATCTGCGCAACCTGCTGGCGGCTACGAAGTGACGTCGGCCACTACTACCTGAAG
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 CCGAAGGGAGGCGCAGGCCTCCCTTCTTTTGGCCGCGCCATGCTCTCCAGCGCCAAACGCCGCGACAGCCTGGACCT
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 GATCTCCAGCGAACTGGAAGATCAGGTCTCAAGCTCGTCCACCCTGAACTGTTCCATGTGCGGAGTTGGTGCTACCTGG
 TCTTCAACATCCTGGTGCAGCTGTTCTGCGCGCGTGCAGGCAATTGCTGCCGATCTTCATCTCGCGCTCACCGACGTG
 CTGATGCTTTGCGGCTGTTCTACGCGAGTGGCGGCGTACCCAGCGGCATCGGCAGCCTGCTGGTGGTGGCGGTGGCCAT
 TGCCAAATCCTGCTGCGCGGGCGCATCGGCCTGGTCATCGCGCGGCGGCCAGCCTCGGCCTGCTTACCTGACCTTCT
 TCCTCAGCCTGAGCAGTCCGGACGCCACCAACCTACGTCCAGGCCGCGGCGCTCGGCACCCTGTGCTTCGCCGCGCG
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 GGAGCTGGTGGCAACCGCCCTACGCTTGGCGCAACCCGGAAGCCGAGGAAGCGCCGGTGGACAACCGCCTGCTCGGCGAGT
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 GGCAGCGGCAAGGAACCTGGTGGCGGCTGATCCAGGAGCAGGGGCCACGTATCGAGCGGCGTTCGTGCCGGTGAAGT
 CGGCGCGATTCCCTCCGAGCTGATGGAAGCGAGTTCCTCGGCCACAAGAAAGCGAGCTTCACTGGCGCTATCGAAGACA

Fig. 2H

AGCAGGGCCTGTTCCAGGCCGCCAGCGGTGGCACCCCTGTTCTCTCGACGAAGTCGCCGACCTGCCGATGGCCATGCAGGTC
 AAAGTGTCTCCGGGCGATCCAGGAAAAGGCCGTGCGCGCGGTGGCGGCCAGCAGGAGGTCCCGTGCACGTGCCCATCC
 TCTGCGCCACCCACAAGGACCTCGCCGCCGAAGTCGGCGCCGGGCGCTTCCGCCAGGACCTCTACTACCGCCTCAACGTC
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 CCGCGAGCTGGAAAAATGCTGGAGCGCGCTATACCCTGTGCGAAGACGACCAGATCCAGCCTCAGACCTGCGCCTGG
 CCGATGCGCCGGGTGCCAGCCAGGAAGGCGCGCGAGCCTGAGCGAAATCGACAACCTCGAGGACTACCTGGAAGACATC
 GAGCGCAAGCTGATCATGCAGGCACTCGAGGAGACCCGCTGGAACCGCACCGCCGCGGCCAGCGCCTGGGCCTGACGTT
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 CAGACGGCACGACGCCGGTGCCAGGACCAGCCCGTTGCGGTAGTGCCCGGTATTAGCCAGAGCCCGTCAAGCCAGGCA
 CCGGACCGATATAGGGGATGCTTTCGGGAGAGCCCGGCGCAACCTGCCAGTGGGCCACCGGTGCATGTCCGCCAGT
 TCCGGCAACAGTTCTGCCGAGACGCCCTGAGGCTTTCAGCGCCTCGTCGGTCCGGCTTGTGCGAAGCCCGAATGTTT
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 GGCACCGCCGCGTAGGCCTCTCGATCGGCACCTTCTTCAACGGCCGGGTGTGGTTGCGTGCCACTGCAAGTGCCTCGGT
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 CCAGGGCCGGGTAGAAGTCTGCGACAGTGGCCAGGGCGGTACCGCCGGGTGTAGCGCCACGGATAGAGCGGCGAG
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 CAGCTCCCGGGCGGTCAACAGGCCGATGACGCCAGCGCCTACCACTACTACATCTCTACTACCCACAGGGCTCCTACCGA
 TTTGCCAGGAACAGAGAAATATCACTCAAAGGGATCAGATGCTGACGAATTGCCTGCTTCAACGAACCTCAGTCAATCTA
 GTCCCGGTGAAAAGCCCATCATACCCGAGAGGTATTCATCCCATGAAATCGAGTGGTTTGAATTTGGTGGAATATCGA
 TAGTCTATCGATCCTTGCGATAGGCGTGACAATTGCGCTGCCACCCTCCCCGACAGAATGAAGCGGACATTAGCCGT
 GATATTGGTGACAGCCTGACTAGTCATGTGATGGCTGCGCGGGCTAGCAGCATAAGAACGGCGTGATCATCGAGGTGTG
 CGGTAGCGGTGACGGCAGTACCTGCAGCGAGGAATGGCATCTCGGTGGTTAGCCGTAAACGACAGGAGCCAACAGATAC
 TGGCCCCGCGATGAAAATACGAGTCGCACCGATATTATTGGCGGGGCTTCGACAAGCGACTGCGCTACCTGCCTAATGGC
 ACCAGCCCTACAGGTAACGGGCGTTTCTTCAATGTAAGGACGATCGCATCGAGTGGCAATTGGTGCTCAATCGGCAAGG
 CCGCCTCAGGGTGGCGGGAAAGAGCGAAAATAAAAGCTCTCTTACCTGTGCTCCAGGCGGTGAGAGAACTGTTTACAT
 ACCGTTTGCCAGTCACTCCACTCTCGCTCCGGCTGTCTGTCTACAGGGACAATGCGCTCTCCACTAGGCAAGATTATC
 TGGCCCTTTTCTTGTGGAGTACTGCATGCGCTCTATTTGTGCGAGCGCCGGCTTTTCCCTGATCGAGTTGATGATGGTG
 TTGGTTCTGGTGCCTATATTGCCAGCATTGCCGTACCCAGTTTCAACGCCTTGATCGAGCGCAACCGAATCCAGACTGC
 CAGCGAGGAACTCTACAGCCTGCTTCAGTACGCTCGCAGCGAAGCTGTAAACCGTCATGCCAATGTGAGCATCAGGGCGA
 CGCAGAAACATGACTGGGCAAAAGGCTGGAATCATCAGCGGCGCGACCACCGTGCAAAAGCACCAAGGTTTCCAGCAG
 GTCTCGCTATCCGCCAGCAGTGGCACTGCGGAGCTGACCTTCAACGCTACCGGCACACTTAGCAACAGGCTGCAACAT
 TGACATAAAGGTCTGCTTCGCCGGTGACAAAAGTACAGGACGTCTGCTTACCGTTACGCCCAGTGAGCGCGTGATCCTGT
 ACCCATCTTCAAAGCAACGGGACAGCTGTAAGTACAGGAAAGCCCATGTCTCGAGAAACGGGTTTACGATGATCGAAGTA
 CTGGTTGCTCTGGTGCTGATCAGCATTGGCGTACTGGGCATGGTTGCCATGCAAGGGCGCACGATCCAGTACACGAGGA
 GTCGGTACAACGCAATGCCGAGCAATGCTTGCTAGCGACCTGATGGAATAATGCGTGCGGACCCAGATGCCGTACTCA
 ATCTACGCGCCCACTACGCGAAGACTCGGTCTACTACAAGGCCAAGGGCAGCGACTTTCCCGCAGCCCCAGCGCGCTGC
 GCGCCATTGCCAGCAGATGCTAAGGAACGTCTCGGTGCTGGGCCCCAACAGGCCTCGAAAGACTTGGCCGGAGCCTCCGC
 ACTCTTGAATAGCCAATTCTACATTTGTCGAGCCCAACCCCGGTACCTGCGACAACACCAAGGCTCGGCCATCGAAA
 TCCAGGTTGCCTGGCGAGCCATGGATGGAGCGTGTTCACGCCTCTGACTCCACCTTGTGACCTACAGCGTCCGCTCC
 GAATTGTGAGAACAGCATGCTCTTACGAAAATGCAGAAAGGCCTATCGATGGTAGAAGTCTGCTGGCACTCGCTATA
 AGCAGCTTCTGATCCTGGGGATCAGCCAGATCTACATCGACAACAAACGCAACTATCTTTTCCAGCAAGGCCAGGCCGG
 CAACCAGGAAAATAGCCGCTTCGTTCTTATGCTGCTGCAGCAACAACTGGATAAGACAGCCTATCGTCGCTTACGACG
 ACAACATGGAGAATGCTTTCAAATCCGCGACATTCAATGGCTGTGCTGCAATTTGTGGTGGCGAGACTATCGCTGCGGCA
 ACTGCCCTCAAGGCGGTGAGTACGGTGTCTGCTTGGCTATCAACCCGCTCAAAAGGGAGCATGATTGCCTCGGTAA

Fig. 21

TGAAATTACCGGAGTTCGGGAAAAGCCCTTCACAAATACTCCCCCTGTCGTCGTTGCGCTGGTCTACCTACCGAGCGCCG
 GTACCTGAGTTGCAGTCGTCCCGATATCGCCAGTCGAAATCGGGAGAATTGGTCAGTGGTCTCACAGACTTCCGCTTG
 GAAGCGGGGTCGGGCCAGCAGATCGTAGCGAACGCAAAGTATCCAGCTTCGTGCGACTACAGGATGTCGCCGGTTCGTCC
 TATCCGAGCATTCGCTTCTCAATCCTGGCAGGCAGCGACAATAACAAGCCTGCGCACAGGAGATGATAGCCAGGCACGCG
 ATCGCTGGATCGTCTTTATCCCGAGAGCAAAGCGCCATCGAGGCCGAGACAAAGGCCAGATTTACCAAATAGCGCGT
 GGTAACCAAACCATCAGGAATCTCATGCCATGACCCTGCGCCATACCTCTCGACAGCAGGGATCCACGTTGTTGATCTCG
 CTGTTTATCTTTGTTGATGATCAGCTCCTCGCCGTTTCCAACATGCGCGAGGTGTCACTGGAAAGCCGTATCACCGGCAA
 TCTCATCGAACAGAAGCGCCTGCGCAATGCGGGCGAAGCTGGGCTACGCGAAGGTGAACGACGCTTTTTTCAATACCATCA
 AGCCCCAGAGGTGCGCAGCGGATGCGCCGATAGCAATGTCAAACGGCCTTGCACTACTGAACCTGAGTGCCCTCTCCGTA
 CCCCAGATGACGTGCACAACAATCCGGTGGCAGCCCTGAACGGCAAGACAGATAACGCCAATTCACGTGTCTGGATGCC
 CTACCGAGGCAGCGATCTGAATAACCTACGCAGATCGACAAAGACCGCGCAGTCACCTGGCAGACCATCACGGTGCCCG
 CTGGCGAACAGAACAAAGAGCGGAAAATCCCGAGTACGGCAACATGATGCGCGGGGTGCGCACGTTCTACTACGAAACC
 AACAGCCGCGCCCTCAACAAGCGGGGCGAGAGACTGTTCTACAGGCCGTTTCATGCACGCTGTATACCAACTGACTGGA
 GCCAGCGCATGATCCACCAGATTACCCGCGCAGGAAAAAGCCTGCTGGCTGCAGGTTGCACCCTGAGCATCCTGTTTCGCC
 TCTGACAGTTATGCCGCCACGGCCCTGAATGTGAGCCAGCAACCCCTGTTCTTAACCCAGGGCGTTGCTCCCAACCTGCT
 GTTCACTCTAGATGACTCAGGCAGTATGGCCTGGGCTTACGTGCCCGACGGTATTAGCGGGAATAGCGGCAGAGCGGGAC
 GTTCCAGCGATTACAACGCAGTGTACTACAACCCCGATTATGCTTACCAAGTGCCCAAGAAATTGACACTGTCAGGCGAT
 CAGATCATCGTTTCCGACTATCCAGTGCCACGCTTCACAGCAGCCTGGCAGGATGGCTACGCCCAAGGCTCCACCACCAA
 CCTGAGCAATAACTATCGCCCTCAATGGGGAACCGGCTGGCTTGGTTGCATCGATAGCAGCTGCAATACCGGGAGAGCTT
 ATTACTATACTTATAAGGTAAGCGCTAGCTGCCCTGCACAGCCGGTGAGCAGCTCCAACCTCTGTTATACCTACAATGCT
 CTTCTTACCAGTCAGGAAAGCAACTTTGCGATATGGTACTCTACTATCGCAACCGCATCCTGGCCACAAAGACCGCTGC
 CAACCTGGCCTTTTACAGCCTGCCGAAAACGTGCGTCTCACTTGGGGGGCCCTGAACACCTGTAGCATCGCGCCCAACA
 GCAGAAGCTGCCAAAACAATGCCCTGCTCCAATTCAACAAGCAGCACAAAATCAATTTCTTCAATTGGCTGGCGAACAGC
 CCGGCCAGCGCGGTACTCCTCTGCATGCGGCTCTTGACCAGCCGGACGCTTCTTGCAACCAACGGCACAGCTTATAC
 CACCGAAGACGGAAAGACATATTCTTCCGCGGCCAGCTATCATATGATGACCGACGGTATCTGGAACGGTCGGAACG
 TCACCCCCGGCAATCTCGACAACCAAGACAGCCTTTCTGATAGCACCTCTATAGGCCACAGCCCCCTTATGCCGAC
 AGCAATGCCAGCTCATTGGCTGACCTGGCTTCAAATACTGGACCACAGACTTACGTCCCAGCATCGACAATGACCTGAA
 GCCTTTTCATGGCTACAAGAGTGGGGACGATTCCAAGGATTACTGGGACCTTCGCAACAACCCAGCCACTTGGCAACACA
 TGGTCAACTTTACCGTTGGCCTAGGTCTTTCTTATTGCTCACATTGAACTCTGCACCAACTTGGACAGGCAGCACCTTT
 GGCAACTACGAGGAGTTGATGGCTGGAAGCAAGGCTTGGCCAGCGTCGATAACGACGCCGACCCGGTAACGTCTACGA
 CCTCTGGCATGCAGCTATCAACTCTCGTGGAGACTTCTTTAGCGCGGAATCACCGGACTCTTGGTTTCAAGCTTTCAATA
 AGATCCTGACACGGATTTCCGAGCGCAACACCTCCTCCTCCAAACAGCAATGACTTCCGCGCTGCAGGATGACGGAACC
 GCGGACAAGCTGATCCGCTACAGCTACAGTCCAGCTTTGCCAGTGACAAGAACTGGCGGGCGACCTTATACGTTACAA
 GGTGGAGTCGACTTCCACCGGTTGCAACAAAACCCAGGAATGGAGCGCCGGCGCACTGCTGGACAACCGAGCTCCCGCTA
 CCCGTAATATTTACATCGCCAGCAATAGCGGAACCAACCGCCTTAAGCCTTTACATGGAGCAATATTGAGGGAAGTCAG
 TTAGCCACTTGGCTGAACCGCAACCCGGACAAGGACAATCAGGCCGACACCAAAGGAGCACAGCGGGTCGACTTCATCCG
 TGGCCAGCAGAATATGGATGGATTCCGGCAACGACAGGCGGTGTTAGGGGACATCGTGCACCTCGTCTCCAGCCGTGGTCG
 GACCGGCCCAATACCTCACTTATCTGGCCAACCCATCGAACCCAGCGGCGACTACGGCACATTCAAGACAGAGGCAGAC
 CAGCGCAGCCCTAGAGTTTATGTTGGATCCAACGATGGCATGTTGCATGGTTTCAACATCAAAACCGGCGTGGAAAGATT
 CGCTTTTCATCCCTACAGCAGTATTCGAAAAGCTTAACAAGCTTACCGGCATCAGCTACCAGGGCGGTGCCCAACAATATT
 TCGTCGACGCTACACCGGTCTGTCAGCGATGCCCTTTTCGATGGAGCTTGGCACACTGTTCTGATCGGAACGCTTGGTGCT
 GGAGGTCGCGGCTGTTTCGCACTCGATGTAACCAAGCCGGACGATGTCAAGCTGCTTTGGGAATACGATAGCAGTACCGA
 CTCGGACCTTGGTTACACTTCTCAAACCTACCGTAGCCAGACTGCACAGCGGACAATGGGCGAGTGTACCGGCAACG
 GCTATGGAAGCGATAATGACAAGGCAGCTTTACTGCTGATTGATTTGAAAAAGGGAACGCTGATCAAGAAGCTGGAAGTC
 CAAAGCGAGCGCGGAATAGCCAATGGCCTATCGACGCCTCGCTGGCTGATAACAACAGCGATGGCATTGCTGACTACGC
 CTATGCTGGCGATCTGCAGGGAATATCTGGCGCTTCGATTTGATCGGCAATACCCGCAACGACGCCAGACACAAATA
 CCTCTATCAATCCCTTCAAGCCCGGAGATGTAGATCCTTCTGCTTTCAGAGTATCGTTTACGGCGCCCCGCTTTTCCGT

Fig. 2J

GCTCGCGCCGACAACAATACTCGTCAGCCCATCACGGCTCCGCCTACCTTGGTACGCCATCCTAGCCGTAAGGGCTACAT
 CGTCATCGTAGGTACAGGAAAATACTTCGAGGACGATGACGCTCAGGCCGATACCAGCCGAGCCATGACGCTCTATGGTA
 TCTGGGATCGCCAGACCAAGGGCGAAAGCGCAAACAGTACCCCAACCATCGACCGCAACGCCCTCACAGCCCAAACCATG
 ACAACAGAGGGCAACTCCACATTCCGGTAGCGTGAACAGGAATATTCCGGCTTATTAGCCAAAACCCGGTGAAGTGGTACAA
 AGACGGAGCAACCGGTACCGGAACTCGGATGTGGCTAGCTATGGCTGGCGACTGAATCTGGAGGTCAATAGCAGCAAGA
 AAGGCGAAATGATGATCGAAGATATGTTGCTGCCGGCCAAGTGCTTCTATTGCAGACCTTGACACCGAACGACGACCTT
 TGTGACAGCGGCTCTACCAGCTGGACCTACGGCCTCAATCCATATACTGGCGGACGTACCAGTTTCACCGTCTTCGATCT
 CAAACGTGCGGGTATAGTGGACTCTGGCTCGGATTACAACGGCTCGGTGCTATCCGCCTTCCAACAGGATGGACTAGGTG
 GCTTGGCCATTACCCAGAACGAACAGCGTCAATCCGAGGCTTGCACTGGTGATGAGTGCATCATCTTCAACCCCAAGCGAC
 AAGAGTAACGGACGACAAACCTGGCGGGTCTGTCGAGGAGAAATGAACATGAACCCCTTACGTCTTCTCGCCACAGCTCTT
 GCAGCTCTAGCTCTGGCTTGGCCAACTTTGCCTTGAGTGCCACGAATACGTTTCGAGAATGTGGGCGTGGTTCGAGGATGT
 TCATCTTGGCCCGGTCTGGTAGTAGTCGATGGGCAGACATATCGCTTGGCCAAACCGTGTCCAACAACAGGACTCGCCGG
 TCATATTCTTGGTACGTGAGGACAGACAGTGTCTTCTCGGCAAACTCACCAGCGACCTGCCAGAAATCGAGTCGTTT
 TACATTATCAAGCAGGCCCCCTCTCGTCCCTTCGGATCGGAGCAGCAACAATGAAGTGAACAGAGGCTTCACTCTCATC
 GAGTTGATGATCGTCGTAGTAATCATCGCTATTCTTGCTGGTATCGCCTACCCAGCTACGACGAATACGTGAAGCGCGG
 GAATCGCACCGAAGGACAGGCATTACTCAGCGAAGCAGCCGCTACTCAAGAGCGCTATTTTTTACAGAACAATACTTATA
 TCACTACCCAAGCCGACATCGGCAAGCTGCATATGCGCAACACATCGGGCACCACAGTGAAGTCCTCCACAGGCAATAC
 AGCCTTACCGTCGATACGGTAGCCAACGACGGAGGTTATCGCCTTATCGCTAACAGGCATTCAACGATCTTGATTGTGG
 CAACCTGACCTTGACCGCAACGGCGAGAAAGGCCGACTGGAAGCAAGAAGAGCGTTGCAGAAATGCTGGCGCTAAAGCG
 CCGAGACAAGAAAAAGGCAAGGCCGGCATAAGCCGGGCTTTTTTCAGGTGCGCAAAAATTCCGATTACAAAGCCTTGACC
 CGCAGTTCCCTTGGGCATCGAGAAGGTAATGTTCTCCTCCCGTCCCTCCAGTTCCCTGCTCTTCCGACGCCCCCACTCAGG
 TAGCTGGGCGATCACTCCGCGCACCAGCACTTCCGGCGCGGAGGCGCCTGCGGTGATTCCGATGCGACGCACACCGTCCA
 ACCAGCCGCGTTGCATGTCTCGGCGCCGTGATCAGGTAGGCCGGCGTGGCCATGCGCTCGGCGAGTTTCGCGCAGGCGG
 TTGGAGTTGGAACGTGTTGGGGCTGCCCAACCACAGGACCATGTGCGACTGGTTCGGCCAGTTCCCTTACGGCATCCTGGCG
 GTTCTGGGTGGCATAGCAGATGTGCTTCTTGGCGGGCCCTGGATCTGCGGGAACCTGGCGCGCAGGCGATCGATGACCT
 TCGAGGTGTGCTCCATCGACAGGGTGGTCTGGGTACGTAAGTGCAGGGCTTCGGGCTTGGCACCTCCAGCGCGGCGACG
 TCGGCTTCTGCTCCACAGGTAGATGGCACCGCGTGTGGCATCGTACTGGCCCATGGTGCCTTCCACCTCGGGGTG
 GCCTTCATGCCCATCGACACGCATTCTGCGGCTGTCGCGGCTGTAGCGCACCCTCCATGTGCACCTTGGTCACAGCG
 GGCAGGTGCGCTCGAAAACCTTCAGGCCGCGCCCTCGGCTTCTTGGGACCGCCTGGGAAACGCGTGGGCGCTGAAG
 ATGACGATGACGTTGTCCGGCACCTGATCGAGTTCCTCGACGAAGATGGCGCGCGCTGGCGCAGGTTGTCCACGACGAA
 CTTGTTGTGCACACCTCGTGACGCAGTAGATCGGCGGGCCGAAGACATCGAGGGCAGGTTGACGATCTCGATGGCGC
 GATCCACGCCGGCGCAGAAGCCGCGGGGATTGGCGAGTTTGATTGATGCGGGTCTCGTGGGCGACGCGGTGATTGGAC
 GAATGAACCTTGCTACCGCCCTCCCCGCTTGGGAAGGGCGCAGCGACCGGTTACAGGCCGGCTGGACGTCGAT

Fig. 2K

>ORF2 (SEQ ID NO:2)

TCGCCGATCCAATGCCAAGGAGTACCTGGGCAATCAGAGCCTACTCACGGCTGCCGGGGCCGGCATTGCCAAGCTCCTGG
ACGCCGACGAGAACAACACCAGTACCGTCTTCAGCGGCAACGGCACCAGCTTCGGGACGACCGGAACCAACAGCAACTCG
GCCCTCAACAGCATCCTCTCCGGCGGGCGTCAGCGACATCCGGCAGTGGATGAACAAGTTGTACGGGGAGGCCTTCGCCGC
CGTCTACGTGCAGCCAGGTGCGCGGGTCGCAGTGCATCTCGATCAGCAACTGGCGATCGACTATGA

>ORF3 (SEQ ID NO:4)

CGCCGATCCAATGCCAAGGAGTACCTGGGCAATCAGAGCCTACTCACGGCTGCCGGGGCCGGCATTGCCAAGCTCCTGGA
CGCCGACGAGAACAACACCAGTACCGTCTTCAGCGGCAACGGCACCAGCTTCGGGACGACCGGAACCAACAGCAACTCGG
CCCTCAACAGCATCCTCTCCGGCGGGCGTCAGCGACATCCGGCAGTGGATGAACAAGTTGTACGGGGAGGCCTTCGCCGCC
GTCTACGTGCAGCCAGGTGCGCGGGTCGCAGTGCATCTCGATCAGCAACTGGCGATCGACTATGAACCAAGGGCCGCA
GGTCGATTACAGCTCTGGAGCCGCTCATGCAACAGCAGACTTGGACTAA

>ORF602c (SEQ ID NO:6)

TCCGCTGGTCATTTCGGGAGGCATCCTGCTGCGGATCGATTGGGCGCCGAGCGTTTGCCTGGCATCGAGGAGCAGCCG
GCCACGGCTGTTGCCATCGAGCTGGTCGCACCTCGCTCCCAGACGTCGAGCATGTTGGCCTCGCCGTGGGGCAGCATCT
CCTCCTTGCTGGTGGAGCAGCTGCCAGGGTCAGCGCGCAGGCCAGGCCGGCGCAGAGACGAAGAAGGGGTTAGTCCAA
GTCTGCTGTTGCATGAGCGGCTCCAGAGCTGTAATCGACCTTGCGGCCCTTGAGTTCATAGTCGATCGCCAGTTGCTGAT
CGAGATGCACTGCGACCCGCGCACCTGGCTGCACGTAGACGGCGGCGAAGGCCTCCCCGTACAACTTGTTTCATCCACTGC
CGGATGTCGCTGACGCCCGCGGAGAGGATGCTGTTGAGGGCCGAGTTGCTGTTGGTTCCGGTCGTCCCGAAGCTGGTGCC
GTTGCCGCTGAAGACGGTACTGGTGTGTTCTCGTCGGCGTCCAGGAGCTTGGCAATGCCGGCCCCGGCAGCCGTGAGTA
G

>ORF214 (SEQ ID NO:8)

ACAAGTTGTACGGGGAGGCCTTCGCCCGCTCTACGTGCAGCCAGGTGCGCGGGTCGCAGTGCATCTCGATCAGCAACTG
GCGATCGACTATGAACCAAGGGCCGAAGGTCGATTACAGCTCTGGAGCCGCTCATGCAACAGCAGACTTGGACTAACCC
CCCTTCTTCGTCTCTGCGCCGGCCTGGCCTGCGCGCTGACCTTGGCAGCGTGCTCCACCAGCAAGGAGGAGATGCTGCC
CACGGCGAGGCCAACATGCTCGACGTCTGGGAGCGAGGTGCGACCAGCTCGATAGGCAACAGCCGTGGCCGGCTGCTCCT
CGATGCCAGGCAACGCTGCGCGGCCAATCGATCCGCAGCAGGATGCCTCCGCAATGACCAGGCCGACTACACCCGCA
CGGCCAGCAACGAGATCCACAGTCAGTTCAAACGACTGCCAATCCCGACCTGGTGATGTATGTGTTCCCGCACCTGGCC
GGCAGCGATCCCGCCCCGTACCGGGCTACACCACCGTGTTCCTTCTACCAGCGAGTCCAGTACGCCATGCCGGGCGA
ACGCACGGAGGACTATTGA

>ORF1242c (SEQ ID NO:10)

TCTCGTCTGGGCGTAGAACTGGACAATCCAGGGTGAGGTTTTCGTGCTCGTCGAAGGAGTTCTGCAGGGCTTCTTTCAAT
GCGTCCCGGGCGTTCTGCATCCAATTGGGATCGCGGCCCTCGGTGCCCAAGGGCACCAGTTCGAAGAATGCCGCGCGCGA
ACGCCATCCTCCAGGAGCATCACTTGCTCGTCGGGCGAGTACTCAGCCAGGGCAGCAGGTCTACGAACGATGGGTCTG
GATCGTAGAGGCGTGACGCTTCGGCCTGCGTGGCGCCATTCTTGCTCCCGGTGTTGGGCAGAGGAATACCCATGGCGGCC
AGTCGCGCCAGATAGCGCTCAGTCGCTTCTTCGCGGGCCGCTACGTCCAGCGCTCCTGAATCTTCGGGAGCGTCTGCCGG
TACCGACTGAGGCTGTGTGCGACCGCGCAGAAGGGTTTGAAGGAGCCCATCAATAGTCTCCGTGCGTTGCGCCGGCAT
GGCGTACTGGACTCGCTGGTAGAAGGGGAACACGGTGGTGTAGCCCGGTACCGGGGCGGGATCGCTGCCGGCCAGGTGCG
GGAACACATACATCACCAGGTGGGATTTGGGAGTCGTTTGAACGACTGTGGATCTCGTTGCTGGCCGTGCGGGTGATG
TCGGCTGGTCATTGCGGGAGGCATCCTGCTGCGGATCGATTGGGCGCCGAGCGTTTGCCTGGCATCGAGGAGCAGCCG
GCCACGGCTGTTGCCATTCGAGCTGGTCGCACCTCGTCCCAGACGTGAGCATGTTGGCCTCGCCGTGGGGCAGCATCT
CCTCCTTGCTGGTGGAGCAGCTGCCAGGGTCAGCGCGCAGGCCAGGCCGGCGCAGAGACGAAGAAGGGGTTAGTCCAA
GTCTGCTGTTGCATGAGCGGCTCCAGAGCTGTAATCGACCTTGC GGCCCTTGA

Fig. 3-1

>ORF594 (SEQ ID NO:12)

CCAGGCCGACTACACCCGCACGGCCAGCAACGAGATCCACAGTCAGTTCAAACGACTGCCCAATCCCGACCTGGTGATGT
ATGTGTTCCCGCACCTGGCCGGCAGCGATCCCGCCCCGTACCGGGCTACACCACCGTGTTCCTTCTACCAGCGAGTC
CAGTACGCCATGCCGGGCGAACGCACGGAGGACTATTGATGGGCTTTTTCAAACCTTCTGCGCGGTTCGCACACAGCCT
CAGTCGGTACCGGCAGACGCTCCCGAAGATTAGGAGCGCTGGACGTAGCGGCCGCGGAAGAAGCGACTGAGCGCTATCT
GGCGCGACTGGCCGCCATGGGTATTCCTCTGCCCAACACCGGGAGCAAGAATGGCGCCACGACGGCCGAAGCGTCACGCC
TCTACGATCAGACCCATCGTTCTGTAGACCTGCTGCCCTGGGCTGAGTACCTGCCCGACGAGCAAGTGATGCTCCTGGAG
GATGGGCGTTTCGCGCGCCGATTCTTCGAACTGGTGCCCTTGGGCACCGAGGGCCGCGATCCCAATTGGATGCAGAACGC
CCGGGACGCATTGAAAGAAGCCCTGCAGAACTCCTTCGACGAGCAGCAAACTCACCCTGGATTGTCCAGTTCTACGCCC
AGGACGAGATCAGCTGGGACAATTTCCAGGAGCAGTTGAGGCAGTACGTCATCCTCGAGCGCGAGGATCGGCCTTCAGC
GAGATGTACCTGGCGCTCATGAAGCATCACCTGGAGGGCATTTCGAAGCCGGGCGGACTGTTCTGTGACACCGCCGTGAG
CAAGCTGCCCTGGCGAGGACAACAGCGCCGCGTGCAGTGGTCTGTCTACCGCCGATCCGCAAGGAGGATGCGCAGATTC
GCGGACAGGACCCGGCGGCGTACCTGAAATCCATCTGCGAGCGTATCCAAGCGGCCCTGGCGAACGCCGGCATCTGTGCT
TCGCGCATGGGCGGACAGGAGATCAGGAACTGGTTGATCCGCTGGTTCAACCCGCACCCGGATCACCTCGGCCAGGCCGA
GGCGGACCTACGTCGCTTCTACGAACTGGTATGCCGTCCGGACGAACCGATCCTGCAGGATGAATTGCCACTGGCCGACG
GCACTGACTTCTCCAGAACCTGTTCTATCGGCAGCCTGTTTCCGATGCCACCCAGGGCGTATGGCTCTTCGATGCCATG
CCGACCCGAGTGATTGTGGTCGACCAAGTTGAACAAAGCGCCGCTGACAGGCCACTTCACCGCGGAGACGCTCAAAGGCGA
TGGCCTCAACGCCCTGTTGATCGAATGCCCGAGGACACGCTGCTGTGCATCACCATGGTCGTGACGCCCGCAGGACATGC
TGAAGGGCATCTGCAGCAGCTCTCGAAAAAGGCCGTTGGTGACACCCAGGCCTCGATCCACACCCGCGAGGACGTGGCC
ACCGTTGACGCCGTGATCGGCCGGGAGCACAAGCTCTATCGCGGAGCGATCGCTCTGTTCTGTGCGCGGCCGCGACCATA
CCAGTTGGAGGAACGCTGCATCACCTGAGCAACGTAAGTCTGCTCGCGCGCCGCTGGTGCCGGTGAACCCGAGAACGAAG
TCGGACCGCTGAACAGCTACCTGCGCTGGCTCCCTCAAACCTTCGATCCAAACGAGAAGCGAGCCCTGGAGTGGTACACC
CAGATGATGTTTCGCTCAGCACATCGCCAACTGTGCGCCATCTGGGGGCGCACACCCGGTACCGGACACCCCTGGCTTCAC
GCTGTTCAACCGTGGCGGCGCGCCGTTGACCTTCGACCCGTTCAACAAGCTGGACCGGCAGATGAATGCCACCGGCTTCA
TCTTCGGGCCAACTGGCTCCGGCAAGTCGGCGTCCCTGACCAACCTCATCTGCCAGATGCTCGCCATGTACCTGCCCGG
ATGTTCTGTGCGGAAGCGGGCAACAGCTTCGGCCTGTGGCCGACTTAGCCAAGCGGTTTGGCCTCTCGGTCCACCGGGT
GCGCCTCGCCCCGGGCTCCGGCGTCAAGCTGGTTCGCGGACGCCATCAAGCTGGTTCGAGAGCCCCGACCAAGTGA
AGGTGCTGGACGCCGAAGACATCGAGGCCTCGACTCGGTCCAGGGCAGCAAGGCCGACCTCGAGGACGACACGAGAC
ATCTGGGCGAGATGGAGATCGTCCCGCCTCATGATTACCGGTGGCGAAGAGAAGGAAGATGCGCGCCTGACCCGTGC
CGATCGCAGCGCCGTCCGCCAGGCGATCCTGGCGGCGCCAGGACCTGCGCGCCGCGGAACCCGACGGTACTGACCCAAG
ACGTGCGCGATGCGCTCTACGAGGCCTCCAGGAGCGATAGCACCGCGCCAGAACGCCGCGCGCGGATCGCCGAAATGGCG
GAAGCCATGCAGATGTTCTGCATGGGCGCCGACGGCGAGATGTTCAATCGCGAAGGCACGCCCTGGCCTGAGGCCGACCT
TACCGTGGTGGATTTGCAACGTACGCGCGCGAAGGCTACGCGCCGAGCTCGGGATCGCTACATCTCGCTGCTGAACA
CCGTGAACAACATCGCCGAACGCGACCAAGTTCAAGGGCCGCGCAATCGTCAAGATCACCAGTGGGGGCACATCATCACC
AAGCACCCGCTGCTGCTGCCCTACGCCATGAAGATCACCAAGATGTGGCGGAACTGGGCGCCTGGTTCTGGCTCGCCAC
CCAGAACATCGACGACATCCAGCCTCCGGGGCGCGATGCTGAACATGATCGAGTGGTGGTTGTGCCTGAACATGCCCC
CCGACGAAGTAGAGAAGATATCCAGGTTCCGCGAGCTGTCGCCGGCGCAGAAGTCGATGATGCTCTCGGCCCGAAGGAA
AGCGGCAAGTTCACCGAGGGCGTCTCCTGGCCAAGGGCAAAGAATACCTCGTCCGTGTGGTTCCCCGAGTCTTACCT
GGCCTGGCCATGACCGAAAACGAAGAAAAGAACCAGCGCTACAACATCATGCAAGCCACCGGCTGCGACGAGCTCGAGG
CGGCCTTGCAAGTCGACGCGGATCTCGACAAGGCGCGCGCCTGCCACCCTTCCCCATTGTTTTCCAGACCAACCGGCA
GTGGAGTGCCAGGACGAATGA

>ORF1040 (SEQ ID NO:14)

GTACCTGCCCGACGAGCAAGTGATGCTCCTGGAGGATGGGCGTTTCGCGCGCCGATTCTTCGAACTGGTGCCCTTGGGCA
CCGAGGGCCGCGATCCCAATTGGATGCAGAACGCCCGGGACGCATTGAAAGAAGCCCTGCAGAACTCCTTCGACGAGCAC
GAAACCTCACCCTGGATTGTCCAGTTCTACGCCAGGACGAGATCAGCTGGGACAATTTCCAGGAGCAGTTGAGGCAGTA
CGTCCATCCTCGAGCGCGAGGATCGGCCTTCAGCGAGATGTACCTGGCGCTCATGAAGCATCACCTGGAGGGCATTTCGA
AGCCGGGCGGACTGTTCTGTGACACCGCCGTGAGCAAGCTGCCCTGGCGAGGACAACAGCGCCGCGTGGGATGGTCTGT
TACCGCCGGATCCGCAAGGAGGATGCGCAGATTGCGGACAGGACCCGGCGCGTACCTGAAATCCATCTGCGAGCGTAT
CCAAGGCGGCCTGGCGAACGCCGGCATCGTCTTCGCGCATGGGCGGACAGGAGATCAGGAACTGGTTGATCCGCTGGT
TCAACCCGCACCCGGATCACCTCGGCCAGGCCGAGGCGGACCTACGTGCTTCTACGAACTGGTATGCCGTCCGGACGAA
CCGATCCTGCAGGATGA

Fig. 3-2

>ORF1640c (SEQ ID NO:16)

GTCCGCCCTCGGCCTGGCCGAGGTGATCCGGGTGCGGGTTGAACGACGGATCAACCAGTTCCTGATCTCCTGTCCGCCCA
TGCGCGAAGCGACGATGCCGGCGTTCCGCCAGGCCGCTTGGATACGCTCGCAGATGGATTTAGGTACGCCGCCGGGTCC
TGTCCGCGAATCTGCGCATCCTCCTTGGCGATCCGGCGGTAGACGACCATCCGCACGCGGCGCTGTTGTCTCGCCAGGG
CAGCTTGTGACGGCGGTGTCGACGAACAGTCCGCCCGGCTTCGAAATGCCCTCCAGGTGATGCTTCATGAGCGCCAGGT
ACATCTCGCTGAAGGCCGATCCTCGCGCTCGAGGATGGACGTAAGTGCCTCAACTGCTCCTGGAAATTGTCCCAGCTGATC
TCGTCCTGGGCGTAGAACTGGACAATCCAGGGTGA

>ORF2228c (SEQ ID NO:18)

GGGGAGCCAGCGCAGGTAGCTGTTACGGGTCCGACTTCGTTCTGCGGTTGACCGGCACCAGGCCGGCGCCGAGCAGTA
CGTTGCTCAGGGTGATGACGCGTTCCCTCAACTGGGTATGGTCGCGGCCCGGCACGAACAGAGCGATCGCTCCGCGATAG
AGCTTGTGCTCCCGGCCGATCAGGCGTCGAACGGTGGCCACGTCTCGCGGGTGTGGATCGAGGCCTGGGTGTACCAAC
GGCCTTTTTCGAGAGCTGCTGCAGATGCCCTTCCAGCATGTCCTGCGGCGTCACGACCATGGTGATGCACAGCAGCGTGT
CCTCGGGCATTGATCGAACAGGGCGTTGAGGCCATCGCCTTTGAGCGTCTCGCCGGTGAAGTGGCCTGTGACGGCGCT
TTGTTCAACTGGTCGACCACAATCACTCGGTGCGGCATGGCATCGAAGAGCCATACGCCCTGGGTGGCATCGGAAACAGG
CTGCCGATAGAACAGGTTCTGGGAGAAGTCAGTGGCGTCGGCCAGTGGCAATTATCTGCAGGATCGGTTCTGTCGGAC
GGCATACCAGTTCGTAGAAGCGACGTAG

>ORF2068c (SEQ ID NO:20)

AGCTTGTGCTCCCGGCCGATCAGGCGTCGAACGGTGGCCACGTCTCGCGGGTGTGGATCGAGGCCTGGGTGTACCAAC
GGCCTTTTTCGAGAGCTGCTGCAGATGCCCTTCCAGCATGTCCTGCGGCGTCACGACCATGGTGATGCACAGCAGCGTGT
CCTCGGGCATTGATCGAACAGGGCGTTGAGGCCATCGCCTTTGAGCGTCTCGCCGGTGAAGTGGCCTGTGACGGCGCT
TTGTTCAACTGGTCGACCACAATCACTCGGTGCGGCATGGCATCGAAGAGCCATACGCCCTGGGTGGCATCGGAAACAGG
CTGCCGATAG

>ORF1997 (SEQ ID NO:22)

CACCCAGGCCTCGATCCACACCCGCGAGGACGTGGCCACCGTTCGACGCTGATCGGCCGGGAGCACAAGCTCTATCGCG
GAGCGATCGCTCTGTTCTGTCGCGGGCCGCGACCATAACCCAGTTGGAGGAACGCTGCATCACCTGAGCAACGTAAGTCTC
GGCGCCGGCCTGGTGGCGGTGCAACCGCAGAACGAAGTCGGAACCGCTGAACAGCTACCTGCGCTGGCTCCCTCAAACCT
CGATCCAAACGAGAAGCGAGCCCTGGAGTGGTACACCCAGATGATGTTCTGCTCAGCACATCGCCAACCTGTGCGCCATCT
GGGGGCGCACCACCGGTACCGGACACCTGGCTTCACGCTGTTCAACCGTGGCGGCGCGCGCTTGACCTTCGACCCGTTT
AACAAGCTGGACCGGCAGATGAATGCCCACGGCTTCATCTTCGGGCCAACTGGCTCCGGCAAGTCGGCGTCCCTGACCAA
CCTCATCTGCCAGATGCTCGCCATGTACCTGCCGCGGATGTTCTGTCGCGGAAGCGGGCAACAGCTTCGGCCTGCTGGCCG
ACTTAGCCAAGCGGTTTGGCCTCTCGGTCCACCGGTGCGCCTCGCCCGGGCTCCGGCGTCAGCCTGGCGCCGTTTCGCG
GACGCCATCAAGCTGGTCGAGAGCCCCGACCAAGTGAAGGTGCTGGACGCCGAAGACATCGAGGCCTCGGACTCGGTCCA
GGGCAGCAAGGCCGACCTCGAGGACGACGAGACATCCTGGGCGAGATGGAGATCGTCGCCCGCCTCATGATTACCG
GTGGCGAAGAGAAGGAAGATGCGCGCTGACCCGTGCCGATCGCAGCGCGTCCGCCAGCGGATCCTGGCGGCGGCCAGG
ACCTGCGCCGCGCGAACCACGCGTACTGACCCAAGACGTGCGCGATGCGCTCTACGAGGCCTCCAGGAGCGATAG

>ORF2558c (SEQ ID NO:24)

GTCGGCCAGCAGGCCGAAGCTGTTGCCCGCTTCCGCGACGAACATCCGCGGCAGGTACATGGCGAGCATCTGGCAGATGA
GGTTGGTCAGGGACGCCGACTTGCCGGAGCCAGTTGGCCCGAAGATGAAGCCGTGGGCATTATCTGCCGGTCCAGCTTG
TTGAACGGGTCAAGGTCAACGGCGCGCCGACGGTTGAACAGCGTGAAGCCAGGGTGTCCGGTACCGGTGGTGGCCCC
CCAGATGGGCGACAGGTTGGCGATGTGCTGAGCGAACATCATCTGGGTGTACCACTCCAGGGCTCGCTTCTGTTTGGAT
CGAAGTTTGA

Fig. 3-3

>ORF2929c (SEQ ID NO:26)

AGCGCATCGCGCACGTCTTGGGTGAGTACCGTGCAGTTCGCGGCGGCGCAGGTCTGGCCGCCCGCAGGATCGCCTGGCG
 GACGGCGCTGCGATCGGCACGGGTGAGGCGCGCATCTTCTTCTCTCGCCACCGGTAATCATGAGGCGGGCGACGATCT
 CCATCTCGCCAGGATGTCTCGCTGGTCTCTCGAGGTGCGCCTTGCTGCCCTGGACCGAGTCCGAGGCCTCGATGTCT
 TCGGCGTCCAGCACCTTCACTTGGTGGGGCTCTCGACAGCTTGATGGCGTCCGCGAACGGCGCCAGGCTGACGCCGA
 GCGCGGGGCGAGGCGCACCCGGTGGACCGAGAGGCCAAACCGCTTGGCTAAGTGGCCAGCAGGCGCAAGCTGTTGCCCG
 CTTCCGCGACGAACATCCGCGGCAGGTACATGGCGAGCATCTGGCAGATGAGGTTGGTCAGGGACGCCGACTTGCCGGAG
 CCAGTTGGCCCGAAGATGAAGCCGTGGGCATTCTGCGCGGTCCAGCTTGTGAACGGGTGCAAGGTCAACGGCGCGCC
 GCCACGGTTGAACAGCGTGAAGCCAGGGTGTCCGTACCGGTGGTGCAGCCCGCAGATGGGCGACAGGTTGGCGATGTGCT
 GA

>ORF3965c (SEQ ID NO:28)

GCGCCTGTTGGGCGGTATCAGGCTGTGGATGTTGTTGCAGCCATTTCATCAAGAGCTGCTTTATCTGCGGGACGATATCC
 CGGCGATCGACTGCCCTCAGTTGAATCTGCTGCAGTCTCTATCAGTACAGGAGCGCATATCCTTAGCGTCTGCAGGGC
 ATCTCTTCGGGGTCTGCAGGATCTGGGTGAGGTTGTCGATCAGGTTCTGGGTGAGCGAATTGAGAACTCTCATTCGTC
 CTGGCACTCCACTGCCGGTGGTCTGGGAAAACAATGGGGAAGGGTGGCAGGCGCGCGCCTTGTGAGATCCGCTGCGA
 CCTGCAAGGCGCCTCGAGCTCGTCGAGCCGGTGGCTTGCATGATGTTGTAGCGCTGGTCTTTTCTTCGTTTTCGGTC
 ATGGCCAGGGCCAGGTAGAGACTCGGGGAACACACGAGCAGGATATTCTTGGCCTTGGCCAGGAGCACGCCCTCGGT
 GAACTTGCCGCTTCTTCTGCGGGCGAGAGCATCATGACTTCTGCGCGCGGACAGCTCGCGGAACCTGGATATCTTCT
 CTAATTCGTGCGGGGGCATGTTGAGGCACAACCACTCGATCATGTTGAGCATCGGCGCCCCGGAGGCTGGGATGTGCG
 TCGATGTTCTGGGTGGCGAGCCAGAACAGGCGCCAGTTTCCGCCACATCTTGGTGATCTTCATGGCGTAGGGCAGCAG
 CAGCGGGTGCTTGGTGATGATGTGCCCTCATCGGTGATCTTGACGATTGGCCGGCCCTTGAAGTGGTCGCGTTCGGCGA
 TGTGTTGTTACGGTGTTCAGCAGCGAGATGTAGGCGATCCGAGCTGGGCGCGTAGCCTTCGCGCGCGTACGTTGCGAAA
 TCCACCACGGTAAGGTGCGCCTCAGGCCAGGGCGTGCCTTCGCGATTGAACATCTCGCCGTGCGCGCCCATGCAGAACAT
 CTGCATGGCTTCCGCCATTTCCGCGATCCGCGCGCGCGTCTGCGCGCGGTGCTATCGCTCCTGGAGGCCTCGTAGAGCG
 CATCGCGCACGTCTTGGGTGAGTACCGTGCAGTTCGCGCGCGCGCAGGTCCTGGCCGCGCCAGGATCGCCTGGCGGACG
 GCGTTCGATCGGCACGGGTGAGGCGCGCATCTTCTTCTCTTCCGCCACCGGTAATCATGAGGCGGGCGACGATCTCCAT
 CTCGCCCAGGATGTCTCGCTGGTCTCTCGAGGTGCGCCTTGCTGCCCTGGACCGAGTCCGAGGCCTCGATGTCTTCGG
 CGTCCAGCACCTTCACTTGGTTCGGGGCTCTCGACAGCTTGATGGCGTCCGCGAACGGCGCCAGGCTGACGCCGGAGCCC
 GGGCGAGGCGCACCCGGTGGACCGAGAGGCCAAACCGCTTGGCTAA

>ORF3218 (SEQ ID NO:30)

GGGGCAGATCATACCAAGCACCCGCTGCTGCTGCCCTACGCCATGAAGATCAGCAAGATGTGGCGGAACTGGGCGCCT
 GGTCTGGCTCGCCACCAGAACATCGACGACATCCAGCCTCCGGGGCGCCGATGCTGAACATGATCGAGTGGTGGTTG
 TGCTTGAACATGCCCCCGACGAAGTAGAGAAGATATCCAGGTTCCGCGAGCTGTGCGCGCGCAGAAAGTGCATGATGCT
 CTCGGCCCCGAAGGAAAGCGGCAAGTTACCGAGGGCGTCTCTGCGCAAGGGCAAAGAATACCTCGTCCGTGTGGTTC
 CCCCAGTCTCTACCTGGCCCTGGCCATGACCGAAAACGAAGAAAGAACAGCGCTACAACATCATGAAGCCACCGGC
 TGGCAGGAGCTCGAGGCGCCTTGCAGGTGCGAGCGGATCTCGACAAGGCGCGCGCCTGCCACCCTTCCCCATTGTTTT
 CCCAGACCAACCGGCAGTGGAGTGCCAGGACGAATGAGAGTTCTGAATTCGCTGACCCAGAACCTGATCGACAACCTGAC
 CCAGATCCTGCAGAACCCCGAAGAGGATGCCCTGCAGACGCTAAGGATATGCGCTCCTGTACTGATAGAGGAGCTGCAGC
 AGATTCAACTGAGGGCAGTCGATCGCCGGGATATCGTCCCGCAGATAAAGCAGCTCTTGGATGAATGGCTGCAACAACAT
 CCACAGCCTGATACGGCCCAACAGGCGCTCATTGAGGCGGTGACCGCGCGGAGATCTACAGCGGAGGCAAGCGTGA

>ORF3568 (SEQ ID NO:32)

CCGAAAACGAAGAAAGAACAGCGCTACAACATCATGCAAGCCACCGGCTGCGACGAGCTCGAGGCGGCGCTTGCAGGTC
 GCAGCGGATCTGCAGAAAGCGCGCGGCTGCCACCCTTCCCCATTGTTTTCCAGACCAACCGGCGAGTGGAGTGCCAGGA
 CGAATGAGAGTTCTGAATTCGCTGACCCAGAACCTGATCGACAACCTGACCCAGATCCTGCAGAACCCCGAAGAGGATGC
 CCTGCAGACGCTAAGGATATGCGCTCCTGTACTGATAGAGGAGCTGCAGCAGATTCAACTGAGGGCAGTCGATCGCCGGG
 ATATCGTCCCGCAGATAAAGCAGCTCTTGGATGA

>ORF4506c (SEQ ID NO:34)

GTCAATAAGTTTCGTTGTCTTTTCGCACATTTCTCCAGTCGAGCCTGGTCCAGTTCAGGAAAGTCCAATGTGCCGCCAGGCA
 GCGCGCCCCCGTTGCCGGCCGACTGAGCGAAGATCGCATCGATAGCGCTCCAGAAGGCTTTGGCGCCGCTTGGATCCCC
 GCGCACTCCACCAGGCGAGCCTGGTGGCGGGCCGCTCGCCATGCATCTGCAGGGGAAGATGGCGCCAAACCAGGTTAC
 GTCCGGATGGCTGTCTACCCAGCGCTTAAGCCGCGGGGTGTAGACCTTGCAGAAGGGGCACTCCAGGTGCGCGTATTCAT
 TGATCGTCCAGCGCGCTTTTCGCATCGCCGTAGAGGCTGTGGTTGGCTGGCAGGCCCTTACCAGAAGCTCTACCCCTACG
 GCGGATGCAGCCAGCAAGACCAGCAGCAGCCCCGCCAGGGCAGGGCGGGACCTTGAAATCGTTTGGCTGCCAGCCGCC
 CTTCAAGAGTCTCAGCCTTGCCTCCGCTGTAGGATCTCCGCGCGGTCCACGGCCTCAATGAGCGCCTGTTGGGCCGTATC
 AGGCTGTGGATGTTGTTGCAGCCATTTCATCAAGAGCTGCTTTATCTGCGGGACGATATCCGCGGATCGACTGCCCTCA
 GTTGA

>ORF3973 (SEQ ID NO:36)

GGCCGTGGACCGCGCGGAGATCCTACAGCGGAGGCAAGCGTGAGACTCTTGAAGGGCGGCTGGGCAGCCAAACGATTTC
 AGGTCCCGCCCTGCCCTGGGCGGGGCTGCTGCTGGTCTTGTGGCTGCATCCGCCGTAGGGGTAGAGCTTCTGGTGAAGG
 GCCTGCCAGCCAAACACAGCCTCTACGGCGATGCGAAAGCGCGCTGGACGATCAATGAATACGCCGACCTGGAGTGCCCC
 TTCTGCAAGGTCTACACCCCGCGGCTTAAGCGCTGGGTAGACAGCCATCCGGACGTGAACCTGGTTTGGCGCCATCTTCC
 CCTGCAGATGCATGGCGAGGCGGGCCGCCACCAGGCTCGCCTGGTGGAGTGCGCGGGGATCCAAGGCGGCGCCAAAGCCT
 TCTGGAGCGCTATCGATGCGATCTTCGCTCAGTCGGCCGGCAACGGGGGCGGGCTGCCTGGCGGCACATTGGACTTTCTT
 GAACTGGACAGGCTCGACTGGAGAAATGTGCGAAAGACAACGAACCTTATTGACTCAGATATCAAGTTGGACATCGACAT
 TGCACGGTCGAAGGGCATTACAGCGACCCCGACCCCTCGTCATCCGGGACAACCAGACGGGACGAAGCGTGAAGCTTGAAG
 GCATGGCCGACGAGACCACGTTGCTGTGCGCGATAGACTGGCTAGCCAAGGATCTCTAG

>ORF4271 (SEQ ID NO:38)

ACCTGGTTTGGCGCCATCTTCCCCTGCAGATGCATGGCGAGGCGGGCCGCCACCAGGCTCGCCTGGTGGAGTGCGCGGGG
 ATCCAAGGCGGCGCCAAAGCCTTCTGGAGCGCTATCGATGCGATCTTCGCTCAGTCGGCCGGCAACGGGGGCGGGCTGCC
 TGGCGGCACATTGGACTTTCCTGAACTGGACAGGCTCGACTGGAGAAATGTGCGAAAGACAACGAACCTTATTGACTCAG
 ATATCAAGTTGGACATCGACATTGCACGGTCGAAGGGCATTACAGCGACCCCGACCCCTCGTCATCCGGGACAACCAGACG
 GGACGAAGCGTGA

>ORF4698 (SEQ ID NO:40)

GAAATCGGCGAGGATTCCAACATCCCTCTTTTGGTCCTCCAGGATGCCCTGCACTTCACCTGGCAGAACCTCGACCTCCT
 CCCCATCCACAATCTTTACCATCTCTTGTGGCCGGAGCTGGTGAGGCTAAGCCTCAACTCCATTGCCGGCCGAGCATTG
 ATGTAAGTGCTCTCGAGCAAGCGCTCCATGACTTCGACCACTCCTTAATATCAGTTAGCCAGCTACATACAGGAATTATG
 CTACCCAGGACATGCAGGCGTCACCCCTACTTATGTACGTGGCAGCGTTCGATCAGGGCTCGAAAAAATACACCACCTAC
 GAGTTGA

>ORF5028 (SEQ ID NO:42)

TTTCCTGCTGCCCTATCGGAAGTGATCCTGTCTGTCTGTACCTTTCTAGAACCGGTACAGACCCATGCCTCTTCATC
 ACTCCCCCCTGGCCGGCGGCCACCAACGCTGGCCGTTGGCGTACTACTGGTACTGCTGAGCAGCGCGAGTCAGGCCGAA
 ACCTGGGTCATACCGACAAGGCTCATCCGGTCTCTGCCACCGGATCGTCGCGCTTCTGTTTCTGGACGCCAGGAACA
 CCTCGAGGAGCAACTGACTGCGGCCTTGCCCCAGGATCCACAGCATGCTCAAGCGGCGTTTAA

>ORF5080 (SEQ ID NO:44)

AACCGGTACAGACCCATGCCTCTTCATCACTCCCCCCTGGCCGGCGGCCACCAACGCTGGCCGTTGGCGTACTACTGGT
 ACTGCTGAGCAGCGGAGTCAGGCCGAAACCTGGGTATCACCAGCAAGGCTCATCCGGTCTCTGCCACCGGATCGTTCGC
 GCGTTCTGTTTCTGGACGCCAGGAACACCTCGAGGAGCAACTGACTGCGGCCTTGCCCCAGGATCCACAGCATGCTCAA
 GCGGCGTTTAAAGCGATTGTACAAAGCCCCGATGGGCGCCGCTGCAGGCAGAGCTGGTCAAGGCACAACAAGACGTCGC
 CGATGCGTGGAGTCTCGGTGTGAGAAGATCCCTGCCGTAGTAGTCGATAGGCAGTACGTGGTCTACGGCGAACCGGATG
 TTTGCGCGCTCTTGAGCTAATCGCCAAGGCCAGGAGGTGCGCGTGA

Fig. 3-5

>ORF6479c (SEQ ID NO:46)

TTCGTCTCCGTGTCCTTATTGGAAGTCGGTACTGCAGATGAACATCTGCCCTTGGCTGGCAGCAGGAGTAGGGACGCC
 AGAGCGCCAGGCGTCTCCCGTCGACGGCTTGGCTCTTCGGCCAGAGTTGGGAAACACCGCGCAGTTGAGGCTCAGG
 GATGGGGTCAGCTCCTGCCATTTCCCGGTCGAGGCATCGCCCTCTTTCAGCTCGCCCGCCGGCCAGTAGCCGTCCTTGGG
 GGCTGCGCGCATGGGGAGGTAGACGTGGAGCTGGCCGATTGCGGTGGTGATATCGCCGGCGCGCTGGGCGATGACGGCTG
 CCGTCTTGTAGTCGTGGTCTGGTGCAGGAAGCCGCTGCGCGGATAGAGGTTCCCCACATGTCGCCGGAGAAGATTCCA
 CCCACCTCGCGCAGCCCTGGGACCAACGCTTCGGGGTACACCTGCTCGGGAATTCATGCCGCCAGCCAATGGCGTCCAG
 TGTGCTGAGAAAAGTACGGCACAGCGGGACGGTGGCGCCAGGGCAAACGTACCCAGAGGCGCTGGCGAACC GGCTGAACG
 TGGCGCCACCAGGATGGCCGATCACATCCGCTTCTTGAAGCGGCCGATGCTGTTCTCGGCCTTGTAGTTTGTGGTCGCG
 TCATTGCCGGCCTGGGCGAGTGGATTGGTGTACCCAGCGCCGATACCTCGGTCCAGGGGTTGCTCCCGGTATTGCGGTA
 GCTGGAGACGACTGCGTCAGGCACGTAGTGGCGGACCTTGACCGACGTCTTCACTTTGCAGCCATGCGGGCCGAGAGCA
 GCCAGTAACAGATCCCAGACCTTGTATTGAGGCACTGAGGGGAAAGGGTGGAGGAGACGATGGCAGCGCTGTTGATC
 GCGGCCGAGGCCGTGAACGAGAGGCTGAAGGTGGCGGCCGCGCTGCCAGGCGCGGAGGTTGAGGCTGGTCATCAGCGC
 GACCTCTGGCCTTGGCGATTAGCTCAAGAGCGCGCGAAACATCCGGTTCGCCGTAG

>ORF5496 (SEQ ID NO:48)

GCTAATCGCCAAGGCCAGGAGGTGCGCTGATGACCAGCCTCAACCTCCGCCGCTGGCAGCGGGCGGCCACCTTCAG
 CCTCTCGTTCACGGCCTCGGCCGCGATCAACAGCGCTGCCATCGTCTCCTCCACCCTTTCCCTCAGTGCCCTGAATACA
 AGGTGCTCGGGATCTGTTACTGGCTGCTCTGCGGCCCGCATGGCTGCAAAGTGAAGACGTGGTCAAGGTCCGCCACTAC
 GTGCCTGACGCAGTCGTCTCCAGCTACGCGAATACCGGGAGCAACCCCTGGACCGAGGTATCGGCGCTGGGTACACCGAA
 TCCACTCGCCAGGCCGCGCAATGACGCGACACAACTACAAGGCCGAGAACAGCATCGGCCGCTTCAAGGAAGCGGATG
 TGATCGGCCATCCTGGTGGCGCCACGTTTCAAGCGGTTTCCGAGCGCCTCTGGGTACGTTTGCCTTGGCGCCACCGTCCC
 CTGGTGGCGTACTTTCTCAGCACACTGGACGCCATTGGCTGGCGGCATGGAATTCGAGAGGTTGACCCGAAGCGTT
 GGTCCCAGGGCTGCGCGAGGTGGGTGGAATCTTCTCCGGCGACATGTGGGGGAACCTCTATCCGCGCAGCGGCTTCTTGC
 ACCAGACCGACGACTACAAGACGGCAGCCGTCATCGCCAGCGCGCCGGCGATATCACCACGCGAATCGGCCAGCTCCAC
 GTCTACCTCCCCATGCGCGCAGCCCCAAGGACGGCTACTGGCCGGCGGGCGAGCTGAAAGAGGGCGATGCCTCGACCGG
 GAAATGGCAGGAGCTGACCCCATCCTGAGCCTCAACTGCGCGGTGTTTCCCAACTCTGGGCCGAAGACGCAAGCCGTCG
 ACGGGGAGCAGCCTGGGCGCTCTGGCGTCCCTACTCCTGCTGCCAGCGCAAGGGGAGATGTTTATCTGCAGTACCGAC
 TTCCAATAA

Fig. 3-6

>ORF5840 (SEQ ID NO:50)

CGCGACCACAACTACAAGGCCGAGAACAGCATCGGCCGCTTCAAGGAAGCGGATGTGATCGGCCATCCTGGTGGCGCCA
CGTTCAGCCGGTTCGCCAGCGCCTCTGGGTACGTTTGCCCTGGCGCCACCGTCCCGCTGGTGCCGTACTTTCTCAGCACA
CTGGACGCCATTGGCTGGCGGCATGGAATCCCCGAGCAGGTGTACCCCGAAGCGTTGGTCCCAGGGCTGCGCGAGGTGGG
TGAATCTTCTCCGGCGACATGTGGGGGAACCTCTATCCGCGCAGCGGCTTCTGCACCAGACCGACACTACAAGACGG
CAGCCGTCATCGCCAGCGCGCGCGGCGATATCACACGCGAATCGGCCAGCTCCACGTCTACCTCCCCATGCGCGCAGCC
CCCAAGGACGGCTACTGGCCGGCGGGCGAGCTGAAAGAGGGCGATGCCTCGACCGGGAATGGCAGGAGCTGACCCCATC
CCTGAGCCTCAACTGCGCGGTGTTTCCCAACTCTGGGCCGAAGACGCAAGCCGTCGACGGGGAGCACGCCTGGGCGCTCT
GGCGTCCCTACTCCTGCTGCCAGCGCAAGGGGCAGATGTTTATCTGCAGTACCGACTTCCAATAAGGACACGGAGACGAA
TCATGCGAATGAACATCACCTCGGTGCGCTAATGTGGCTGCTCGCAGCGCAACTTGCCAGGCCGACGACCCGATCAAC
GTGTCCAAGACCGGCACGGTGTCTAGCGACGAGGTCTCTACAGCATTGGCGGCGGAGTGCGGTGAGCATGGGCAGCGC
CGGCCAGATGGACTCGATCGCGCTCGGCTTCCGCTGGAACAACGACATGATGTGCGGAAACATGAACCTGAGCACACCCC
TGGAGAACCAGCTCAACGGTGCCACACAGGGTTTCCAGAACATCATGGGCTCAGTCATCCAGAACGCGACCGGCGCGGT
ATGTGCTGCCGGCGTTGATCATCCAGCGCGCAACCCCTCAGCTCTACAACCTGATACCAATGGCATCCTGCAGGCGCG
GATCGACTACGACCGCTCGAAAGGGACTTGCAAAACGATCGCCGAAAAGATGGCTGACATCGCTGGCGAGCAGACCGGCT
GGGGGAAAATCGCCGAAGGCCAAGCCCTGGGCGCCACACTGGCCTCTGACGGGAAAGACGCCGTATCCGCCCTCGAAGCA
GTGGAGAAGAAAGGCGGCAACGATGGCGTAACCTGGGTTGGTGGAGACAAGGCCGGCGGCTCCGGCCAGAAGCCCATTCG
CATCGTCAACGACGTGACCCGGGCGGGCTACAACCTGTTGACGACCGCTCGGTGAATGATTTCGTGAGCGTGCCTTCCG
CCACTTGCAACAACGGCCTGGTCTGCAACACTTGGTCTCCCCCAGGAGGCCCGGCATTGCCACCCGGGTACTGGGG
GAGCAACAGCAACAGACCTGCCAAGGCTGCCAGAAGACGGTGACGGCTGCTGGCGTCGGCCTCACCCCGCTGATCCAGGA
GACCTACGACAAGAAGCTCCAGTCGCTGCAGGAGCTGCTGTGCAAGAGCAAACCACTGACTGCAGAGAACCTGGCTGCGG
CCGGCACCGATGCTCTGCCAATTACCCGCGCGTCATCGAGGCGCTGCGCGACGAGCGTGACCAGGACGTCTGGCGCGC
CGCCTGGCGTCCGATGTCTCCCTGATGGACGTGCTCAGCAAGGCACTGCTACTGCAGCGCCTGATGTTTCGCCGGCGCCAA
GGAGCCCAACGTGCGCGCAACGGCCTGGCCACCCAAGCCGTCGATCAGCAGACCAGCCTCCTGCAGCAGGAGATCTCCA
ATCTCAAGACCGAACTGGAATCCGTGCGGAGTTGGCCAGCAACTCCCCATGCGGGTCATCGAGCGCGGGAACAACGC
GCCTCAGGGTCCAGTGGCGTGTTCGAGTCGGCGCCCGATGCCGATCGCCTCGATCGCCTGCAGGCCCCCTCTGCCGCCGG
CGGCAAGTCGGGAGGGAGACCGTGA

>ORF5899 (SEQ ID NO:52)

TCCGCCATCCTGGTGGCGCCACGTTTCAGCCGGTTCGCCAGCGCCTCTGGGTACGTTTGCCCTGGCGCCACCGTCCCGCTG
GTGCCGTACTTTCTCAGCACACTGGACGCCATTGGCTGGCGGCATGGAATTCGAGCAGGTGTACCCCGAAGCGTTGGT
CCCAGGGCTGCGCGAGGTGGGTGGAATCTTCTCCGGCGACATGTGGGGGAACCTCTATCCGCGCAGCGGCTTCTGCACC
AGACCGACGACTACAAGACGGCAGCCGTATCGCCAGCGCGCCGGCGATATCACCAAGCGAATCGGCCAGCTCCACGTC
TACCTCCCCATGCGCGCAGCCCCAAGGACGGCTACTGGCCGGCGGGCGAGCTGA

>ORF6325 (SEQ ID NO:54)

GCCTCAACTGCGCGGTGTTTCCCAACTCTGGGCCGAAGACGCAAGCCGTCGACGGGGAGCACGCCTGGGCGCTCTGGCGT
CCCTACTCCTGCTGCCAGCGCAAGGGGCAGATGTTTATCTGCAGTACCGACTTCCAATAAGGACACGGAGACGAATCATG
CGAATGAACATCACCTCGGTGCGCTAATGTGGCTGCTCGCAGCGCAACTTGCCAGGCCGACGACCCGATCAACGTGTC
CAAGACCGGCACGGTGTCTAGCGACGAGGTCTCTACAGCATTGGCGGCGGAGTGCGGTGAGCATGGGCAGCGCGGGC
AGATGGACTCGATCGGCGTGGGCTTCCGCTGGAACAACGACATGATGTGCGGAAACATGAACCTGAGCACACCCCTGGAG
AACCAGCTCAACGGTGCCACACAGGGTTTCCAGAACATCATGGGCTCAGTCATCCAGAACGCGACCGGCGCGGTGATGTC
GCTGCCGGCGTTGATCATCCAGCGCGCAACCCCTCAGCTCTACAACCTGATACCAATGGCATCCTGCAGGCGCGGATCG
ACTACGACCGCTCGAAAGGGACTTGCAAAACGATCGCCGAAAAGATGGCTGA

Fig. 3-7

>ORF7567c (SEQ ID NO:56)

CAGTGCCTTGCTGAGCAGTCCATCAGGGAGACATCGGACGCCAGGCGGCGGCCAGGACGTCTGGTCACGCTCGTCGC
GCAGCGCCTCGATGACGCCGCGGGTAATTGGCAGAGCATCGGTGCCGGCCGAGCCAGGTTCTCTGCAGTCAGTGGTTTG
CTCTTCGACAGCAGCTCCTGCAGCGACTGGAGCTTCTTGTCGTAGGTCTCCTGGATCAGCGGGGTGAGGCCGACGCCAGC
AGCCGTACCGTCTTCTGGCAGCCTTCGAGGTCTGTTGCTGTTGCTCCCCAGTACCCGGGTGGCGAATGCGGCGGCCT
CCTGGGGGGAGGACCAAGTGTTCAGACCAGGCCGTTGTTGCAAGTGGCGGAAGGCACGCTCGACGAATCATTACCCGAG
CGGCTGGTCAACAGGTTGTAGCCCGCCGGGTACGTCGTTGACGATGCGAATGGGCTTCTGGCCGGAGCCGCCGGCCTT
GTCTCCACCAACCCAGGTTACGCCATCGTTGCCGCTTTCTTCTCCACTGCTTCGAGGGCGGATACGGCGTCTTTCCCGT
CAGAGGCCAGTGTGGCGCCAGGGCTTGGCCTTCGGCGATTTTCCCCAGCCGGTCTGCTCGCCAGCGATGTCAGCCATC
TTTTCGGCGATCGTTTTGCAAGTCCCTTTTCGAGCGGTGCTAGTCGATCCGCGCCTGCAGGATGCCATTGGTGATCAGGTT
GTAGAGCTGAGGGTTCGCGCGCTGGATGATCAACGCCGCGAGCGACATGACCGCGCCGGTCGCGTTCTGGATGACTGA

>ORF7180 (SEQ ID NO:58)

TTCTGTCGAGCGTGCCTTCCGCCACTTGCAACAACGGCCTGGTCTGCAACACTTGGTCTCCCCCAGGAGGCCGCCGAT
TCGCCACCCGGGTACTGGGGGAGCAACAGCAACAGACCTGCCAAGGCTGCCAGAAGACGGTGACGGCTGCTGGCGTCGGC
CTCACCCCGCTGATCCAGGAGACCTACGACAAGAAGCTCCAGTCGCTGCAGGAGCTGCTGTGGAAGAGCAAACCACTGAC
TGCAGAGAACCTGGCTGCGGCCGGCACCGATGCTCTGCCAATTACCCGCGCGTCATCGAGGCGCTGCGCGACGAGCGTG
A

>ORF7501 (SEQ ID NO:60)

CCAGGACGTCTGGCGCGCCGCTGGCGTCCGATGTCTCCCTGATGGACGTGCTCAGCAAGGCACTGCTACTGCAGCGCC
TGATGTTCCGCCGGCCCAAGGAGCCCAACGTCCGCCCAACGGCCTGGCCACCCAAGCCGTGATCAGCAGACCAGCCTC
CTGCAGCAGGAGATCTCAATCTCAAGACCGAACTGGAACCTCCGTCCGCGAGTTGGCCAGCAACTCCCCATGCGGGTCAT
CGAGCGCGGGCAACAACGCGCCTCAGGGTCCAGTGGCGTGTTCGAGTCGGCGCCCGATGCCGATCGCCTCGATCGCCTGC
AGGCCCCCTCTGCCCGCGCGGCAAGTCCGGGAGGAGACCGTGATGGCAGATACGCTCACCACCCGAAAGCTTCTCGGTC
AGCTACTGGTCCGAGTGCTGATCGTCATCGGACTGGCAGTGGTGGTACGCTGCTCAGTCTCTTCGCCCTGAACCACTTC
GGTGGCATCCAGGGCCTGGAGGCTGGCGGCAAGCAACTACTGGAGCTTGTTCGCCTGGCGGGCGCTGCTGTACTGCGC
CCTGGCCATCGCCTGGTTCCGGCAGCGCAAGGAACTGAGCGCGCATGAGCGGCAGCGCATTGCGCGGATCGAGATCCTGG
TGCTGTTGCTGGTCTGCTCATCGAATTCAGCAAAGCCTACTTCCGCACGGGAGGCGCAGCATGA

>ORF7584 (SEQ ID NO:62)

TGTTCCGGCGGCCAAGGAGCCCAACGTCCGCCCAACGGCCTGGCCACCCAAGCCGTGATCAGCAGACCAGCCTCCTG
CAGCAGGAGATCTCCAATCTCAAGACCGAACTGGAACCTCCGTCCGCGAGTTGGCCAGCAACTCCCCATGCGGGTCATCGA
GCGCGGGCAACAACGCGCCTCAGGGTCCAGTGGCGTGTTCGAGTCGGCGCCCGATGCCGATCGCCTCGATCGCCTGCAGG
CCCCCTCTGCCCGCGCGGCAAGTCCGGGAGGAGACCGTGATGGCAGATACGCTCACCACCCGAAAGCTTCTCGGTACAGC
TACTGGTCCGAGTGCTGATCGTCATCGGACTGGCAGTGGTGGTACGCTGCTCAGTCTCTTCGCCCTGAACCACTTCGGT
GGCATCCAGGGCCTGGAGGCTGGCGGCAAGCAACTACTGGAGCTTGTTCGCCTGGCGGGCGCTGCTGTACTGCGCCCT
GGCCATCGCCTGGTTCCGGCAGCGCAAGGAACTGAGCGCGCATGA

>ORF8208c (SEQ ID NO:64)

AGGTCATGCTGCGCCTCCCGTGCAGGAGTAGGCTTTGCTGAATTTCGATGAGCAGGACCAGCAACAGCACCAGGATCTCGA
TCCGCCGAATGCGCTGCCGCTCATGCGCGCTCAGTTCTTGGCGTGCAGGACCAAGGCGATGGCCAGGGCGCAGTACAGC
AGCGCCCGCCAGGCGAACAAGCTCCAGTAGTTGCTTTGCCGCCAGGCCTCCAGGCCCTGGATGCCACCGAAGTGGTTAG
GGCGAAGAGACTGAGCAGCGTACCGACCACTGCCAGTCCGATGACGATCAGCACTCCGACCACTAG

Fig. 3-8

>ORF8109 (SEQ ID NO:66)

GCGGCAGCGCATTGCGCGGATCGAGATCCTGGTGCTGTTGCTGGTCCTGCTCATCGAATTGAGCAAAGCCTACTTCCGCA
 CGGGAGGCGCAGCATGACCTTCATGACCAATGACTACCTGGAGTATTACCTCACCCTCCTCGGCTGGATCATCAACAACG
 GGATCTGGAACATGATCTCGGATACTGGCCTGTTGCGGGTGGCGTTGCGCGCCATCGTGATGCGCGAATGGCTGAAAGTT
 CGTGGGGAAGGCGCCGACGAGGGCAACAAGGGAGTGCTGTCTCTGCCCCGATCGAGACGCATATCTACGTCGGCTACAT
 CGTGGTCGCGCTGGCGGGATCCCGGTGCTCAACGTGAGCTTCGACACCATCGAGTTCGACCAGACTCGCGCCAGCAGT
 GCCAATACAATCTGCCGGCACCGCGGACACCGGTGGTCGAGCTCCTTCAGCAGCCTGGCCGGCAAGAGTGCGCAGATG
 CCGCTCTGGTGGGCGATGATGCACGCCCTGTCCAAGGGCTTCACCAGCGGCGCCATCGCGGCCATTCCGTGCGGCACGGA
 TCTGCGGCAGATGCGAATGGAAGTGGACAACACGCGCGTGAACAATCCGCTGCTGGCACAAGAAATCGCTGATTTTCCA
 GAGACTGCTACGGGCCTTCCCGTGCGCGGTGTTTCATGCGGCAACCCGACCTGGGCTCCGTGCGCGAGGACAACAAGGCG
 TTGCAAGACCTGAACTGGATCGGCTCCCGATTCTTGTGAACACCCGGGGTACTACGACACCGACTACTCGAAGAGTCC
 CCGTCAGTCGTGGCCCTACAACGCCACCCGCGATGCCGGCTGCCTCAGGTGGGCGGTGGTGGCGGCTACCCAACCTGCA
 AGCAGTGGTGGGCTGACTCAGGGATCGGCTTGGTGATCGGATCAAGGACCAGGTGGATCCGGACCTGATGACCAGCTTC
 CTAAGTGGGCGAAATGGTTGAACCAGGACGAGGTGACCGAGGCTGTATTGCCAGGTGATCTCACCCTCCAGCCAGGT
 CAAGGGTAACGTCTACACCGATTACGGCGGGCAGGTGGGCGGCACCGTGTGGAACGGCATCGCGAGAACCAGGAACT
 TCGGCGTTGCGGTGGGCGAGCTTGGCATACTTCCCGCGATGGATATGGTCCGCCAGGCACTGCCGATGGTGATGTCGTT
 CTGAAGATGGCAATGGTCATCTGCATTCCGATGGTCCTGGTCATCGGCACCTATCAACTGAAAGTTGCCATGACGATGAC
 GGTGCTCTTCTTTCGATGATGTTCTGTCGACTTCTGGTTTCAGTTAGCCAGATATATCGACAGCAGATACTTGATGCTT
 TCTATGGTTTCGGGATCACCACATCTTTCATTCAACCCAGTCATGGGGCTGAATACGGCTACTCAAGATGCGATCTTGAAC
 TTCGTTATGGGTTCTATGTTTATTGTTTTACCACTACTGTGGATGACAGCGATCGGCTGGTCCGGAATTCAAGCAGGGTC
 TGTCTGAACGGATTGAGCAGAGGGACTGAAGGAGTTCAAGCCCGCGCAAGGAAGCAGGAAATAGAGTTAAAAACGCAG
 TTTGA

>ORF9005c (SEQ ID NO:68)

GTCAGCCCACTGCTTGCAGGTTGGGTAGCCGCCACCACCGCCACCTGAGGCAGGCCGGCATCGCGGGTGGCGTTGT
 AGGGCCACGACTACGGGGACTCTTCGAGTAGTCGGTGTCGTAGTACCCCGGGGTGTTCAACAAGAATCGGGAGCCGATC
 CAGTTCAGGTCTTGCAACGCCCTTGTGTCTCGGCGACGGAGCCAGGTGCGGTTGCCGATGAACAGCCGCGCACGGGA
 AGGCCGTTAGCAGTCTCTGGAATAATCAGCGATTTCTTGTGCCAGCAGCGGATTGTTACCGCGCTGTTGTCCACTTCCA
 TTCGCATCTGCCGAGATCCGTGCCGACGGAATGGCCGCGATGGCGCCGCTGGTGAAGCCCTTGGACAGGGCGTGATC
 ATCGCCCAACAGAGCGGCATCTGCCGACTCTTGGCGGCCAGGCTGCTGAAGGAGCTCGACCAGCCGGTGTCCGCCGGTGC
 CGGCAGATTGTATTGGCACTGCTGGGCGGAGTCTGGTGAAGTTCGATGGTGTGGAAGCTCAGGTTGACGACCGGGATCC
 CCGCCAGGGCGACCAAGATGTAGCCGACGTAGATATGCGTCTCGATGCGGGCGAGAGACAGCACTCCCTTGTGTCCTCG
 TCGGCGCTTCCCCACGAATTTTCAAGCATTTCGCGCATCAGATGGCCGCGAAGCGCACCGCGAACAGGCCAGTATCCGA
 GATCATGTTCCAGATCCCGTTGTTGATGATCCAGCCGAGGAGGTGAGGTAATACTCCAGGTAGTCATTGGTCATGAAGG
 TCATGCTGCGCCTCCCGTGCGGAAGTAG

>ORF8222 (SEQ ID NO:70)

CTACCTGGAGTATTACCTCACCCTCCTCGGCTGGATCATCAACAACGGGATCTGGAACATGATCTCGGATACTGGCCTGT
 TCGCGGTGCCGTTCCGCGCCATCGTGATGCGCGAATGGCTGAAAGTTTCGTGGGGAAGGCGCCGACGAGGGCAACAAGGGA
 GTGCTGTCTCTCGCCGCGATCGAGACGCATATCTACGTGCGCTACATCGTGGTGGCCCTGGCGGGGATCCCGGTGCTCAA
 CGTGAGCTTCGACACCATCGAGTTCGACCAGACTCGCGCCAGCAGTGCCAATACAATCTCGCGGCACCGCGGACACCG
 GCTGGTCGAGCTCCTTCAGCAGCCTGGCCGGCAAGAGTGCGCAGATGCCGCTCTGGTGGGCGATGATGCACGCCCTGTCC
 AAGGGCTTCACCAGCGCGCCATCGCGGCCATTCCGTGCGGCACGGATCTGCGGCAGATGCGAATGGAAGTGGACAACAC
 GCGCGTGAACAATCCGCTGCTGGCACAAGAAATCGCTGA

>ORF8755c (SEQ ID NO:72)

CAGTCTCTGGAATAATCAGCGATTTCTTGTGCCAGCAGCGGATTGTTACGCGCGTGTGTCCACTTCCATTTCGATCTG
 CCGCAGATCCGTGCCGACGGAATGGCCGCGATGGCGCCGCTGGTGAAGCCCTTGGACAGGGCGTGATCATCGCCACC
 AGAGCGGCATCTGCGCACTCTTGGCGGCCAGGCTGCTGAAGGAGCTGACCAAGCCGGTGTCCGCCGGTGGCGGCAGATTG
 TATTGGCACTGCTGGGCGGAGTCTGGTGAAGTTCGATGGTGTGGAAGCTCAGTTGACGACCGGGATCCCGCCAGGGC
 GACCACGATGTAG

Fig. 3-9

>ORF9431c (SEQ ID NO:74)

CTGAAACCAGAAGTCGACGAACATCATCGCAAAGAAGACGACCGTCATCGTCATGGCAACTTTCAGTTGATAGGTGCCGA
TGACCAGGACCATCGGAATGCAGATGACCATTGCCATCTTCAGGAACGACATCACCATCGGCAGTGCCTGGCGGACCATA
TCCATCGCCGGGAAGTATGCCAAGCTGCCACCGCAACGCCGAAGGTTCTGCGGTTCTCGCGATGCCGTTCCACACGGT
GCCGCCACCTGCCCGCCGTAATCGGTGTAGACGTTACCCTTGACCTGGCTGGAGGGTGA

>ORF9158 (SEQ ID NO:76)

CGTCTACACCGATTACGGCGGGCAGGTGGGCGGCACCGTGTGGAACGGCATCGCGAGAACCGCAGGAACCTTCGGCGTTG
CGGTGGGCAGCTTGGCATACTTCCCGCGCATGGATATGGTCCGCCAGGCACTGCCGATGGTGATGTCGTTCTGAAGATG
GCAATGGTCATCTGCATTCCGATGGTCTTGGTTCATCGGCACCTATCAACTGAAAGTTGCCATGACGATGACGGTCGTCTT
CTTTGCGATGATGTTCTGTCGACTTCTGGTTTCAGTTAGCCAGATATATCGACAGCAGGATACTTGA

>ORF10125c (SEQ ID NO:78)

GTGATAGCAGGATGCCTCCCTTTGGGAGCCAGGAGATTGATGATGAACGCGCACACCAACAAAGGCTTTGCCTCCCGGAT
CGGTTTTGGTCTGGGTATGCTTGTGCGTTTCTGCCTGCATGATCGCCGTCCAGCTCTACGTTGGGTTAAGCGAGTTAGCC
TATTCTTGTAGTAGCTCTTGTAGTGTACAGAATTTTATGTGGCTTGGTGGGTATCAATGACTCTACTGTGTGCTTTT
CTGGTGGGATTTGCCTTGGTTAAAGGGGACATCTCCGTCTCTAAAGGGTCTCAAGTCGAGATGTCTCAACTATGACTTC
ACAAGCTGAACTGAATCTGTAGCAGAGCTGTTTACTATCAGGCAGCACACCATTACCGGGACTAG

>ORF9770 (SEQ ID NO:80)

TCAAACAGCTCTGCTACAGATTGAGTTTCAGCTTGTGAAGTCATAGTTGAGACATCTCGACTTGGAGACCCCTTTAGAGAC
GGAGATGTCCCTTTAACCAGGCAAATCCACCAGAAAGACACACAGTAGAGTCATTGATACCCAGCAAGCCACATAA
AATTCTGTGACACTACAAGAGCTACTAACAAGAATAGGCTAACTCGCTTAACCCAACGTAGAGCTGGACGGCGATCATGC
AGGCAGAAACGCACAAGCATAACCCAGACCAAACCGATCCGGGAGGCAAAGCCTTTGTTGGTGTGCGCGTTTCATCATCAA
TCTCCTGGCTCCCAAAGGGAGGCATCCTGCTATCACTTACGCCGAAAAAGATGATTTGGCAAGCATTATGGCATATTA
TGCCACTAGCTATCTGCCGACTGGAGTACCTCATGGCAACGCGAAACGTCGTCCTTCCCGATCCGCTGGAGCAGGATATC
AACGAGCTGGTGGAGACCGGCCCTATCAGAATCGCAGCGAAGTCATCCGGGCAGGCTTGCCTGCTGCTGCAACAGGA
AGCCAGATANGCGCAAGCTCGAAACCTCCGCAACGCAACATCCAGTGGGCTGATGCAACTGGAGCGCGGCGAGTACG
ACGAGATCACCAGCGACGAACCTGGCCCAATACCTCGACGAGCTCGGCAACCAGGCGAGCCACTGA

>ORF9991 (SEQ ID NO:82)

AGCTGGACGGCGATCATGCAGGAGAAACGCACAAGCATAACCCAGACCAAACCGATCCGGGAGGCAAAGCCTTTGTTGG
TGTGCGCGTTTCATCATCAATCTCCTGGCTCCCAAAGGGAGGCATCCTGCTATCACCTATACGCCGAAAAAGATGATTTGG
CAAGCATTATGGCATATTATGCCACTAGCTATCTGCCGACTGGAGTACCTCATGGCAACGCGAAACGTCGTCCTTCCCGA
TCCGCTGGAGCAGGATATCAACGAGCTGGTGGAGACCGGCCGCTATCAGAATCGCAGCGAAGTCATCCGGGCAGGCTTGC
GCCTGCTGCTGCAACAGGAAGCCAGATANGCGCAAGCTCGAAACCTCCGCAACGCAACATCCAGTGGGCTGATGCAA
CTGGAGCGCGGCGAGTACGACGAGATCACCAGCGAGAACTGGCCCAATACCTCGACGAGCTCGGCAACCAGGCGAGCCA
CTGAAGCATGGCCAAGTACCGCATCTCTCATGA

>ORF10765c (SEQ ID NO:84)

CACCTGGTCTGTGCGCACCCGGTAGAAGACGAAGTGCCTGGGCCGAACAACCTTACCAGACATTGGGCATCGAGTGGCAGT
AAACGAGGTGGATGCTGCGCAGGCCAGCTCCAGTTCTTACGGCTGATGCTGCCTACCTGTTGTGGGTCTGTGCGAACT
GCTTCCAGCGCCGCCCTATGAGTGCCTGGTAACGTCGGCGCGCGGCATCGCCGAAGTGGTTGTGGGTGAAGCGCAGGAT
ATCGACGATGTCCGCTTGGGCATCATGAGAGATGCGGTACTTGGCCATGCTTCAGTGGCTCGCCTGGTTGCCGAGCTCGT
CGAGGTATTGGGCCAGTTCGTGCTGGTGTATCTGTCGTAATCGCCGCGCTCCAGTTGCATCAGCCCACTGGATGTTGCG
TTGCGGAGGGTTTCGAGCTTGGCGCNTATCTGGCTTCTGTTGTCAGCAGCAGGCGCAAGCCTGCCCGGATGACTTCGCT
GCGATTCTGATAGCGCCGGTCTCCACCAGCTCGTTGATATCCTGCTCCAGCGGATCGGGAAGGACGACGCTTTCGCGTTG
CCATGAGGTACTCCAGTCGGCAGATAGCTAG

Fig. 3-10

>ORF10475 (SEQ ID NO:86)

AGCATGGCCAAGTACCGCATCTCTCATGATGCCCAAGCGGACATCGTCGATATCCTGCGCTTCACCCACAACCACTTCGG
CGATGCCGCGCGCCGACGTTACCAGGCACTCATAGGGGCGGCGCTGGAAGCAGTTGCGACAGACCCACAACAGGTAGGCA
GCATCAGCCGTGAAGAACTGGGAGCTGGCCTGCGCAGCATCCACCTCGTTTACTGCCACTCGATGCCCAATGTCCGGTAAG
GTTGTTTCGGCCAGGCACTTCGTCTTCTACCGGGTGGCGACAGACCAGGTGCTAGAGGTGGTTCGCGTGCTTCACGACGC
CATGGATGTGGATCAACACCTGCCCCAACGATGA

>ORF11095c (SEQ ID NO:88)

AGCCGCATGCAAGCGGTGGTCAGCACGAATGCAAATGCTTGGTCAGGGGGAATGCAATCGAGTGGTCAAGCCACTGCTAT
TGCGCATCAACCATGGGGCACCTGCTGGTGGATGTTACCCGTAGCCTTTTCGTGTTGCGCGGCGCGAACGACGCCCTTT
CTGCCTTCGGCAGGCCCTTTTCGGGTAGGGCTTTTACCCTTGTGAACATTCCCTTCGCCCTTAAGGCCATTTCCTTT
TGGGCCATTGCTCCTGTTACAGTTGCTCATCGTTGGGGCAGGTGTTGATCCACATCCATGGCGTCGTGAAGCACGCGAA
CCACCTCTAG

>ORF11264 (SEQ ID NO:90)

ACCGCGGTGCGGAGAGATCTCCTCAAAGTATGGGTTGCACGCATATCGAAGCAGATTACATAGGAGGCTTGGCTGTTT
AACAGCTCCTGAGGGGACTTGGGTTGCCCATGGTTCCACGGCCCAATCGTTGACGTATTGACGATTCCGCTGGCTTTT
TCAGTACGCATCGCTTGGCGCTCCATTACCCAGCCCAATGCGGCCTTGCGGTTGACCAAGCGATTCCAAGGACTGCGATC
CATGTAGCCAGCCCTTAATGCATGTATGTATAGGTAAGGTGCTCGTTATTTTCGGCGTGGATGTGCTGA

>ORF11738 (SEQ ID NO:92)

GAAGAGGTGATCATGAAGTTACAGGCATATCGGCTGCAGAACTACCGCCGGCTGCGCGATGTTGTCATCGAGCTCGATGA
CGAAATTTCTATCTTTGTCGGTGCCAAACAGCGGGAAGACATCCGCCGTCCAAGGCCTGTACTCAATGCTTCGCGGCG
AAGTGAAGAAAGTTTCGAGCTCTTTGACTTCAGTGCGGCGCTGTGGGCGGAGATCGATGCGGTGCGCAGGACGCCCCCTGGC
GATGAGGATGCGCCAAAAGGTTACCGTCCATACTCTTGGATCTCTGGTTCGCGCTCGGTGAAGACGACCTCGCCACTGC
GATGTCGCTGCTGCCGAGCACTGAGTGGGACGGCAAGTGCGTCCGGGATCCGGGTAGCGTTTCGAGCCTCGGGATGCCACG
AGCTCGTCTGGAAGTTCATGAACATACATGAGAAGGCCAAACAGCAGCTGTGCGCTTGGCGGCAAGCGCAAGGCCGCC
GGGAGCAAGCTGTGGAGGCGGGCGGGAAGACGCGGCTGCGGTGGTGGCCGATGCCGGCGAGTACAAGCCTTGGCCAGA
AAGCCTGACGAAGTACCTCACAAGGAAGTGAAGGAATACACCTTCCGCTACTACGTGCTCGATGAGCGGGCTTTTG
TCGGCTATCAGGCAAGGAGGCGGACTACGAGCCGCTACCCCTAGGCAAGGAGCGGGCGGTGCGAGCCATTCTCAAGTCG
CTGGTGAGGGTGCATTCCTGCGCGCGCAGCGGCACCTCGATGACCAGATGCCGGTAGCTCTGATCGCGCAGAGAGCTT
GTCGCGGCGCTGAGCAGGTTCTATCACCAGCACTGGAGAAGCGTGGCGACGACCATGCGGCTCTCAAGGCGCTAGATA
CCTCGGAGAAGGAGCTGAACTTCCACCTGAAGGAAGTCTTCAATGACACCCTCACGCGCCTGGCCAAGCTCGGCTATCCG
GGCGTCAACAATCCGGAGATCGTGATTTCGGGCGGCTTGGATCCGACCACTGTCTTGGGGCAAGACGCCAAGGTTCACTA
CGTGATCCCGGGCGTAGCTTCGCCCCAACTGCCAGACAGCTACAATGGCCTGGGGTTCAAGAATCTGGTCTACATGGTGG
TTGAGCTGCTCGACTTGACAGGAGTGGAAAGCCGAGGATGACAAGCGAGCTCCGCTTCATTTGGTCTTCATTGAGGAG
CCTGAGGCGCATCTGCACGCGCAGATCCAGCAGGTCTTCATCAGGAACGTTTTGCGCCTCCTTGAGGATGCTAACGATCA
CGCGACTTTGTTCCACAGCAGCTCGTCATCACCAGCACTCCCGCACATCCTCTATGAACGCGGATTCTCGCCCATTC
GGTACTTCCGCCGCGTCAACGACCAGTTGGGCCATCACACGGATGTGCGCAATCTGTCGCTATTCAAAACGGGCGCGTCC
GACGCTCCAGCGCGCAATTCTGACGCGGTATCTGAAGCTGACGCACTGCGATCTCTTTTTTCCGACGCGGTGATATT
GGTGGAAAGGCAACGTCGAGCGTCTGCTCCTGCCTGCAATGATCGAGTTGGTGGCCAAGCGCCTGCGTTCTTCCGCCCTAA
CCATCCTTGAAGTCGGTGGTGCCTGCGCATCGGTTCCAGGAGCTGATCGCCTTCGTTGGGCTCACAACACTGGTCATC
ACGGATCTGGACAGCGTGACGGTCAAGACGAGCGCGAGAAGGCCGCCGCGCAAGGCGCAGGCGCTGAGGGCGCGCTTGA
CGGAGATGACGAGGACGAGGACGACGACCTGAAGCCCTTCGAGCTTGAAGACGACGACGAAGCAGAACCAGTGGCAAGA
AGAAGTCCAAGAAGCGTGGCAGCACCTGCCATGCACAGTGAAGGTGCCGTACGTCCAACCAAAACCTCATCAGCTGG
ATCCCGAAGAAGCGGTGATGGCAGAGCTCTGGGAAGTACGCGCGGAGCAAAAGACGCTGTGCTGGCTGAGGATTCCAG
CGCTGGGGTTTCGGTAGCTTACCAGACCAAGGTTTCGGTGACGGTGGGTGCGACGACATCACAGCTCTGCGGCGCGACAC
TTGAGGAGGCCTTTGGTCTTGAGAACGCGGACTGGTGCCAGGCTGAGGCAACCGGTGCGTTCGCGCTCAAGCTCAAGCGC
GCACCGAGCAGCCCTGAAGAGCTGGCTGAGAAGTTACACGATAGGGTGGTGGCAAGAACTTCGACAAGACCCGCTTTGC
GCTGGAGTACTCGAAGCGGGCGCTCAATGGCTGGAAGGTTCCCGGTACATCGCCGAGGCTTGGCTGGCTCGAAG
CCAAAGTGGCCACGAGCTTGAGGCGGATGCTGCCATCGCCACCGAGGTGCGGACTATTGAGCCGACTACAGCCGATGTT
GTCGCTATCATTGTTGACCCGGGGCAGACGGCATGA

Fig. 3-11

>ORF12348c (SEQ ID NO:94)

CGGAAGGTGTATTCCTTGCTCAGTTCCTTTGTGAGGTACTTCGT CAGGCTTCTGGCCAAGGCTTGTACTCGCCGGCATC
GGCCACCACCGCAGCCGCGTCTTCCGCGCCCGCTCCACAGCTTGCTCCCCGGCGGCTTGGCGTTGGCCGCAAGCGCGA
CAGCTGCGTTGTTGGCCTTCTCATGTAGTTCATGGAACCTCCAGACGAGCTCGTGGGCATCCCGAGGCTCGAACGCTACC
CGGATCCCGACGCACTTGCCGTCCCACTCAGTGCTCGGCAGCAGCGACATCGCAGTGGCGAGGTCTGCTTACCGACGCG
GAACCAGAGATCCAAGAGTATGGACGGTAACCTTTTGGGCGCATCCTCATCGCCAGGGGGCGTCTGCCGACCGCATCGA
TCTCGGCCACAGCGCCGCACTGAAGTCAAAGAGCTCGAACTTCTTCACTTCGCCCGGAAGCATTGAGTACAGGCCTTGG
ACGGCGGATGTCTTCCGCTGTTGTTGGCACCACAAAGATAGAAATTTCTCATCGAGCTCGATGACAACATCGCGCAG
CCGGCGGTAG

>ORF12314c (SEQ ID NO:96)

GGTACTTCGT CAGGCTTCTGGCCAAGGCTTGTACTCGCCGGCATCGGCCACCACCGCAGCCGCGTCTTCCGCGCCCGCC
TCCACAGCTTGCTCCCCGGCGGCTTGGCGTTGGCCGCAAGCGCGACAGCTGCGTTGTTGGCCTTCTCATGTAGTTCATG
GAACTTCCAGACGAGCTCGTGGGCATCCCGAGGCTCGAACGCTACCCGGATCCCGACGCACTTGCCGTCCCACTCAGTGC
TCGGCAGCAGCGACATCGCAGTGGCGAGGTCTTACCGACGCGGAACCAGAGATCCAAGAGTATGGACGGTAACCTT
TTGGGCGCATCCTCATCGCCAGGGGGCGTCTGCCGACCGCATCGATCTCGGCCACAGCGCCGCACTGA

>ORF13156c (SEQ ID NO:98)

CGACAGATTGCGCACATCCGTGTGATGGCCCAACTGGTCGTTGACGCGCGGAAGTACCGAATGGGCGAGAATCCGCGTT
CATAGAGGATGTGCGGGGAGTGCGTGGTGATGACGAGCTGCGTGTGGAACAAAGTCGCGTGATCGTTAGCATCCTCAAGG
AGGCGCAAAACGTTCTGATGAAGACCTGCTGGATCTGCGCGTGACAGTGCCTCAGGCTCCTCAATGAAGACCAAATG
AAGCGGAGCTCGCTTGTATCCTCGGCTTTCCACTGCTCGTGCAAGTCGAGCAGCTCAACCACCATGTAGACCAGATTCT
TGAACCCAGGCCATTGTAGCTGTCTGGCAGTTGGGCGGAAGCTACGCCCGGGATCACGTAGTGAACCTTGGCGTCTTGC
CCCAAGACAGTGGTCGGATCCAAGGCCGCCGAATCACGATCTCCGGATTGTTGACGCCCGGATAGCCGAGCTTGGCCAG
GCGCGTGAGGGTGTCAATTGAAGACTTCTTCAGGTGGAAGTTCAGCTCCTTCTCCGAGGTATCTAG

>ORF12795 (SEQ ID NO:100)

CTTCCGCCCAACTGCCAGACAGCTACAATGGCTGGGGTTCAAGAATCTGGTCTACATGGTGGTTGAGCTGCTCGACTTG
CACGAGCAGTGGAAAGCCGAGGATGACAAGCGAGCTCCGCTTCATTGTTGTTTATTGAGGAGCCTGAGGCGCATCTGCA
CGCGCAGATCCAGCAGGTCTTTCATCAGGAACGTTTTGCGCCTCCTTGAGGATGCTAACGATCACGCGACTTTGTTCCACA
CGCAGCTCGTCATCACACGCACTCCCCGCACATCCTCTATGAACGCGGATTCTCGCCATTCTGGTACTTCCGCCGCGTC
AACGACCAGTTGGGCCATCACACGGATGTGCGCAATCTGTGCTATTCAAACGGGCGCGTCCGACGCTCCAGCGCGCGA
ATTCCTGCAGCGGTATCTGA

>ORF12314c (SEQ ID NO:96)

GGTACTTCGT CAGGCTTCTGGCCAAGGCTTGTACTCGCCGGCATCGGCCACCACCGCAGCCGCGTCTTCCGCGCCCGCC
TCCACAGCTTGCTCCCCGGCGGCTTGGCGTTGGCCGCAAGCGCGACAGCTGCGTTGTTGGCCTTCTCATGTAGTTCATG
GAACTTCCAGACGAGCTCGTGGGCATCCCGAGGCTCGAACGCTACCCGGATCCCGACGCACTTGCCGTCCCACTCAGTGC
TCGGCAGCAGCGACATCGCAGTGGCGAGGTCTTACCGACGCGGAACCAGAGATCCAAGAGTATGGACGGTAACCTT
TTGGGCGCATCCTCATCGCCAGGGGGCGTCTGCCGACCGCATCGATCTCGGCCACAGCGCCGCACTGA

>ORF13156c (SEQ ID NO:98)

CGACAGATTGCGCACATCCGTGTGATGGCCCAACTGGTCGTTGACGCGCGGAAGTACCGAATGGGCGAGAATCCGCGTT
CATAGAGGATGTGCGGGGAGTGCGTGGTGATGACGAGCTGCGTGTGGAACAAAGTCGCGTGATCGTTAGCATCCTCAAGG
AGGCGCAAAACGTTCTGATGAAGACCTGCTGGATCTGCGCGTGACAGTGCCTCAGGCTCCTCAATGAAGACCAAATG
AAGCGGAGCTCGCTTGTATCCTCGGCTTTCCACTGCTCGTGCAAGTCGAGCAGCTCAACCACCATGTAGACCAGATTCT
TGAACCCAGGCCATTGTAGCTGTCTGGCAGTTGGGCGGAAGCTACGCCCGGGATCACGTAGTGAACCTTGGCGTCTTGC
CCCAAGACAGTGGTCGGATCCAAGGCCGCCGAATCACGATCTCCGGATTGTTGACGCCCGGATAGCCGAGCTTGGCCAG
GCGCGTGAGGGTGTCAATTGAAGACTTCTTCAGGTGGAAGTTCAGCTCCTTCTCCGAGGTATCTAG

Fig. 3-12

>ORF12795 (SEQ ID NO:100)

CTTCCGCCCCAACTGCCAGACAGCTACAATGGCCTGGGGTTCAAGAATCTGGTCTACATGGTGGTTGAGCTGCTCGACTTG
CACGAGCAGTGGAAAGCCGAGGATGACAAGCGAGCTCCGCTTCATTTGGTCTTCATTGAGGAGCCTGAGGCGCATCTGCA
CGCGCAGATCCAGCAGGTCTTCATCAGGAACGTTTTGCGCCTCCTTGAGGATGCTAACGATCAGCGCACTTTGTTCCACA
CGCAGCTCGTCATCACCACGCACTCCCGCACATCCTCTATGAACGCGGATTCTCGCCCATTCCGGTACTTCCGCCGCGTC
AACGACCAGTTGGGCCATCACACGATGTGCGCAATCTGTCGCTATTCAAACGGGCGCGTCCGACGCTCCAGCGCGCGA
ATTCCTGCAGCGGTATCTGA

>ORF13755c (SEQ ID NO:210)

GCTACCCGAACCCAGCGCTGGAATCCTCAGCCAGCGACAGCGTCTTTTGCTCCGCCGTGACTTCCAGAGCTCTGCCAT
CGACCGCTTCTTCGGGATCCAGCTGATGAGGGTTTGGTTGGACGTGACGGCACCTTCCACGTGTGCATGGCAGGTGCTGC
CACGCTTCTTGACTTCTTCTTGCCACTCGGTTCTGCTTCGTCTGCTCTCAAGCTCGAAGGGCTTCAGGTCGTCTGTC
TCGTCCTCGTCATCTCCGTCAACGGCGCCCTCAGCGCCTGCGCCTTGCGCGGGCGCCTTCTCGGCGTCCGTCTTGACCGT
CACGCTGTCCAGATCCGTGATGACCAGTGTGTGAGCCCAACGAAGGCGATCAGCTCCTGGAACCGATGCGCGAACGCAC
CACCAGCTTCAAGGATGGTTAGGGCGGAAGAACGCAGGCGCTTGGCCACCAACTCGATCATTGAGGCAGGAGCAGACGC
TCGACGTTGCCCTTCCACCAATATCACC CGCTCGGAAAAAAGAGATCGCAGTGCCTCAGCTTACGATACCGCTGCAGGAA
TTCGCGCGCTGGAGCGTCCGACGCGCCCGTTTGAATAGCGACAGATTGCGCACATCCGTGTGA

>ORF13795c (SEQ ID NO:212)

TGTCGTCGCACCCACCGTCACCGAAACCTTGGTCTGGTAAGCTACCCGAACCCAGCGCTGGAATCCTCAGCCAGCGACA
GCGTCTTTTGCTCCGCCGTGACTTCCAGAGCTCTGCCATCGACCGCTTCTTCGGGATCCAGCTGATGAGGGTTTGGTTG
GACGTGACGGCACCTTCCACGTGTGCATGGCAGGTGCTGCCACGCTTCTTGACTTCTTCTTGCCACTCGGTTCTGCTTC
GTCGTCGCTTCAAGCTCGAAGGGCTTCAGGTGCTGCTCCTCGTCTCCTCGTCATCTCCGTCAACGGCGCCCTCAGCGCCTG
CGCCTTGCGCGGGCGGCTTCTCGGCGTCCGTCTTGACCGTCACGCTGTCCAGATCCGTGATGACCAGTGTGTGAGCCCA
ACGAAGGCGATCAGCTCCTGGAACCGATGCGCGAACGCACCACCGACTTCAAGGATGGTTAG

>ORF14727c (SEQ ID NO:214)

CAGGAAGTCGGCGAGCTGAAGGATGTCTCGTGCCCAAGTATGCCCTTGCGGTAGTCACTGCCCACGCCGTAGTTGAACG
TCCTGACGCCGGCCACAGCCTCCAGGCTTCGGACATATCGCTCTTGGTTCGGCCTTGTTCTGTGCGCGTGGTCTGCCGG
ACACGCGAGCTGTAATTCTCGAACTCTTCTTCAAGTTCGGAGATCCGCCTGCGGATGTGCTTCTGCAGCCAAACCTTGAT
GTCGGCCTGGAACGTCTTTGCAATAGACCAGTAAAAGCTGTGGATGGTTCGAGACATGAACCAGCGGGTCATCGTTGACGT
CCGCCAGGATTTCAATTGGTGGCAAGGTGCGTATACGTGATGCACGCGACTATCTGCTTCTCGCCCGCATGCTGGCGCCG
TGCTCCGAGATCACCAGTCCAGCGCCTTGATGAGGGAGGTGGTCTTGCCGGAACCTGCGCCAGCACGAACCACGAAGGG
CTGCGGAGGCGTCGCTACAATGCATGCGTGGATCTCGCGGTGCGGTGCGTATCTGGGCTATCAATTCGTCTGCTCATGC
CGTCTGCCCCGGGTCAACAATGATAGCGACAACATCGGCTGTAGTGGCTCAATAGTCGCGACCTCGGTGGCGATGGCAG
CATCCGCCCTCAAGCTCGTGGGCCACTTTGGCTTCGAGCCAGGCCAAGCCCTCGGCGATGTACGCGGGAACCTTCCAGCCA
TTGAGCGGCCCGCTTGCAGTACCTCCAGCGCAAAGCGGGTCTTGTGAAAGTTCTTGCCGACCAACCTATCGTGTAACCT
CTCAGCCAGCTCTTCAGGGCTGCTCGGTGCGCGCTTGAGCTTGAGGCCGACCGACCGGTTTGCCTCAGCCTGGCACCAGT
CCGCGTTCTCAAGACCAAGGCCTCCTCAAGTGTGCGGCCGAGAGCTGTGATGTGCTGCACCCACCGTCACCGAAACC
TTGGTCTGGTAA

>ORF13779 (SEQ ID NO:216)

CGGTGGGTGCGACGACATCACAGCTCTGCGGCCGCACACTTGAGGAGGCCTTTGGTCTTGAGAACGCGGACTGGTGCCAG
GCTGAGGCAAACCGGTGGTGGCCTCAAGCTCAAGCGCGCACCAGCAGCCCTGAAGAGCTGGCTGAGAAGTTACACGA
TAGGGTGGTGGCAAGAACTTCGACAAGACCCGCTTTGCGCTGGAGGTACTCGCAAGCGGGCCGCTCAATGGCTGGAAGG
TTCCCGGTACATCGCCGAGGGCTTGGCCTGGCTCGAAGCCAAAGTGGCCACGAGCTTGAGGCGGATGCTGCCATCGCC
ACCGAGGTGCGGACTATTGAGCCGACTACAGCCGATGTTGTGCTATCATTGTTGACCCGGGGCAGACGGCATGAGCAGA
CGAATTGA

Fig. 3-13

>ORF14293c (SEQ ID NO:218)

GGGAGGTGGTCTTGGCGGAACCTGCGCCAGCACGAACCACGAAGGGCTGCGGAGGCGTCGCTACAATGCATGCGTGGATC
TCGCGGTTCGGCGTCGGTATCTGGGCTATCAATTTCGTCTGCTCATGCCGTCTGCCCCGGGTCAACAATGATAGCGACAACA
TCGGCTGTAGTCGGCTCAATAGTCGCGACCTCGGTGGCGATGGCAGCATCCGCCTCAAGCTCGTGGGCCACTTTGGCTTC
GAGCCAGGCCAAGCCCTCGGCGATGTACGCGGGAACCTTCCAGCCATTGAGCGGCCCGCTTGCGAGTACCTCCAGCGCAA
AGCGGGTCTTGTGCGAAGTCTTGGCGACCACCTATCGTGTAA

>ORF14155 (SEQ ID NO:220)

CCCCGGGCGAGCGGCATGAGCAGACGAATTGATAGCCAGATACCGACGCCGACCGCGAGATCCACGCATGCATTGTAGC
GACGCCTCCGCGAGCCCTTCGTGGTTTCGTGCTGGCGCAGGTTCCGGCAAGACCACCTCCCTCATCAAGGCGCTGGACTGGG
TGATCTCGGAGCACGGCGCCAGCATGCGGGCGAGGAAGCAGATAGTCGCGTGCATCACGTATACCGACCTTGCCACCAAT
GAAATCCTGGCGGACGTCAACGATGACCCGCTGGTTTCATGTCTCGACCATCCACAGCTTTTACTGGTCTATTGCAAAGAC
GTTCCAGGCCGACATCAAGGTTTGGCTGCAGAACGACATCCGCGAGGCGGATCTCCGAACCTTGAAGAAGAGTTTCGAGAATT
ACAGCTCGCGTGTCCGGCAGACCACGCGCGACAGGAACAAGGCCGACCAAGAGCGATATGTCCGAAGCCTGGAGGCTGTG
GCCGGCGTCAGGACGTTCAACTACGGCGTGGGCACTGACTACGCCAAGGGCATACTTGCCACAGGACATCCTTCAGCT
CGCCGACTTCCTGCTACAAAACCGCCCGCTGTTCCGACGGGTCTGGCGCTGAGCTACCCGTTCTGTGTTTATCGATGAGA
GTCAGGACACGTTCCCGGGTGTAGTGAAGTCTTCAAGGAAGTGAAGCCAGATGCAGGCAAGTTCTGCCTTGGTTTTT
TTCGGCGACCCGATGCAGTCGATCTTCATGAGAGGCGCAGGGGACATCCAGCTTGAGGATCATTGGCGGGCCATCACGAA
GCCGGAGAACTTTTCGCTGCGCCAAAGCAGATCCTTGACGTCGCCAATGCCGTGCGCGCGCAGGGCGATGGCATGGAGCAAG
TCCGCGGGCTGCACGAGAGGGTCGATGGGAACCTCAAGCTGGTGGAGGGTTCGGCCCGGATGTTCTGTCTTGCCGAACACG
CTGAACCGAACCAGGCTTTGGCAAGAGTCCGAGCGTGGAGCTCGGCGACGAACAACGACGAGGGTTGGACAACCCGAGA
CATCGCAGTCAAGATTCTTGTCTCATCGTGACCCGATGGCCGCAAACCGGCTTGGCTTCGCGCGCATCTACTCGGCGCTGA
ACGACAAGACGTCGGATGCCATGAAGCAAGGGATGCAGGACGGCACCGGTTGGCCCGTTCGACCCCTTCTAAGTTTTGCG
CTACCGATCGTTGCAGCTGTGAAGGCCGGCAATGAGTTTCGCGCGGATGAGCCTGCTCCGGGAATTACGCCCCGCGCTGGC
GCCTGCGGCTCTGACCGGCCGACGTGCCGCGGATGTATTGCGAGAGCTGCACGCTGCTGCGTCGAGGCTTGTGCGCATGC
TGGACGAGGCGAGGACCACCATTGGTGACATAGCTCTCCATCTCTGTGACACGGGTCTTTTTGAGTTTCGACGAGCGCTAT
GCGCGTGTCTTGGGTTTGTGACGGATATTGCTGACACCGCTCAGGAGCCCGAGGCTGCTGATGCAGTTCCGGCCGAAGG
ATTATCCTTGGACGCGACAATGGCCAAGTCTTCAATTGCTCTGCGCAAGAGCTTTGGCCCTATGAACGCTATGTCTCAG
AAGGCTCCCCCTATGCCACGCAGCACGGCGTGAAGGGAGCGCAGTTTCAACGCGTCATGGTGGTATGACGAGGAAGAA
AGCGACTACCGAACGTACAACCTACGAGCGTGTCTTCGCGAGTGTGAGGCCCGCGCTGCAGATCGTGCACGAGCACTAGA
CGGTGATGAAAACACTTGGAGCCGAACGCTGCGACTGCTTTACGCTCTGCTGCACTCGTGGCCAGCGGGGCTGGTACTAG
CGTTCTTTGTGCGCGACCTGCGACCAACCTGGAAAACGTCGTGGCGAGCGGGATCTTGCCGCGAAGCGCAGTCTTTACG
CAGGAAGTGTTAGTTGGATGGCCATAG

>ORF14360 (SEQ ID NO:222)

TCGCGTGCATCACGTATACCGACCTTGCCACCAATGAAATCCTGGCGGACGTCAACGATGACCCGCTGGTTTCATGTCTCG
ACCATCCACAGCTTTTACTGGTCTATTGCAAAGACGTTCCAGGCCGACATCAAGGTTTGGCTGCAGAACGACATCCGCGAG
GCGGATCTCCGAACCTTGAAGAAGAGTTCGAGAATTACAGCTCGCGTGTCCGGCAGACCACGCGCGACAGGAACAAGGCCG
ACCAAGAGCGATATGTCCGAAGCCTGGAGGCTGTGGCCGGCGTCAGGACGTTCAACTACGGCGTGGGCACTGACTACGCC
AAGGGCATACTTGCCACAGGAGACATCCTTCAGCTCGCGACTTCTGCTACAAAACCGCCCGCTGTTCCGACGGGTCGT
GGCGCTGA

>ORF15342c (SEQ ID NO:224)

GAAGGGTCGAACGGGCCAACCGGTGCGGTCCTGCATCCCTTGCTTCATGGCATCCGACGTCCTGTGCTTCAGCGCCGAGT
AGATGCCGCCGAAGCCAAGCCGGTTTGGCGCCATGCGGTGCACGATGACAAGAATCTTGACTGCGATGTCTGGGGTTGTC
CAACCCTCGTCGTTGTTTCGTGCGCCGAGCTCCACGCTCGGACTCTTGCCAAAGCCTCGGTTTCGGTTTCAGCGTGTTCGGCAA
GACGAACATCCGGGCGGACCCCTCCACCAGCTTGAGGTTCCCATCGACCCTCTCGTGCAGCCCGCGGACTTGCTCCATGC
CATCGCCCTGCGCGCGCACGGCATTGGCGACGTCAAGGATCTGCTTGGCGCAGCGAAAGTTCTCCGGCTTCGTGATGGCC
CGCCAATGATCCTCAAGCTGGATGTCCCTGCGCTCTCATGAAGATCGACTGCATCGGGTTCGCCGAAAAAACAAGGCA
GAACCTGCCCTGCATCTGGGCTTCCACTTCCTTGAAAGACTTCACTACACCCGGGAACGTGTCCTGACTCTCATCGATAA
ACACGAACGGGTAGCTCAGCGCCACGACCCGTCGGAACAGCGGGCGGTTTTGTAG

Fig. 3-14

>ORF15260c (SEQ ID NO:226)

ATGCCCGCGAAGCCAAGCCGGTTTGC GGCCATGCGGTGCACGATGACAAAGAATCTTGACTGCGATGTCTGGGGTTGTCCA
ACCCTCGTCGTTGTTTCGTGCGCGAGCTCCACGCTCGGACTCTTGCCAAAGCCTCGGTTTCGGTTCAGCGTGTTCGGCAAGA
CGAACATCCGGGCGGACCCCTCCACCAGCTTGAGGTTCCCATCGACCTCTCGTGCAGCCCGCGGACTTGCTCCATGCCA
TCGCCCTGCGCGCGCACGGCATTGGCGACGTCAAGGATCTGCTTGGCGCAGCGAAAGTTCTCCGGCTTCGTGATGGCCCG
CCAATGA

>ORF14991 (SEQ ID NO:228)

CGTCGCCAATGCCGTGCGCGCGCAGGGCGATGGCATGGAGCAAGTCCGCGGGCTGCACGAGAGGGTCGATGGGAACCTCA
AGCTGGTGGAGGGGTGCGCCCGGATGTTTCGTCTTGCCGAACACGCTGAACCGAACCAGGGCTTTGGCAAGAGTCCGAGCG
TGGAGCTCGGCGACGAACAACGACGAGGGTTGGACAACCCAGACATCGCAGTCAAGATTCTTGTCATCGTGCACCGCAT
GGCCGCAAACCGGCTTGGCTTCGGCGGCATCTACTCGGCGCTGAACGACAAGACGTCGGATGCCATGAAGCAAGGGATGC
AGGACGGCACCGGTTGGCCCGTTTCGACCCTTCCTAAGTTTTCGCTACCGATCGTTGCAGCTGTGAAGGCCGGCAATGA

>ORF15590c (SEQ ID NO:230)

CGCTCGTCGAACTCAAAAAGACCCGTGTCACAGAGATGGAGAGCTATGTACCAATGGTGGTCCCTGCCTCGTCCAGCAT
GGCGACAAGCCTCGACGCAGCAGCGTGCAGCTCTCGCAATACATCCGCGGCACGTCGGCCGGTCAGAGCCGCAGGCGCCA
GGCGCGGGCTGAATTCGGGAGCAGGCTCATCGCCGCGAACTCATTGCCGGCCTTCACAGCTGCAACGATCGGTAGCGCA
AAACTTAGGAAGGGTCGAACGGGCCAACCGGTGCCGTCTGCATCCCTTGCTTCATGGCATCCGACGTCTTGTCGTTTCAG
CGCCGAGTAG

>ORF15675c (SEQ ID NO:232)

TCCTTCGGCCGGAAGTGCATCAGCAGCCTCGGGCTCCTGAGCGGTGTCAGCAATATCCCTGACAAACCAAGAACACGCG
CATAGCGCTCGTCGAACTCAAAAAGACCCGTGTCACAGAGATGGAGAGCTATGTACCAATGGTGGTCCCTGCCTCGTCC
AGCATGGCGACAAGCCTCGACGCAGCAGCGTGCAGCTCTCGCAATACATCCGCGGCACGTCGGCCGGTCAGAGCCGCAGG
CGCCAGGCGCGGGCTGAATTCGGGAGCAGGCTCATCGCCGCGAACTCATTGCCGGCCTTCACAGCTGCAACGATCGGTA
G

>ORF16405 (SEQ ID NO:234)

ATCGACTCTTTGAGGAAATGCGTGGGAAGCCTGGAAGAGTGCTGTTTCGCCTGCAAGAAATAATTTCATGTTTCATGCGAT
TCGTTGTGCGGCAGTGC GGCGAGTCCCAAGGCTGGCGAAGGTTTCATGAGCTCTCCAACCTCAGTAGTTGCGTTGGTCCCTTA
GCCTTTTATCAATCGCTGCCACAAAACCTGTGGAGCGATTGTTTCGATGCCAGCGAGCAGAGCTACAAATCTCCATCACG
GGTGGTGATTACAAAGCTGCCAGCTTATGTTGACCAATAACGGGTCAAAGCCTGCAACTTTAGTTTCCTTCGAAATCAC
ATCGAAAGCCACGACCAATACGAAAACATGGTTTTTGGTAAGCAATACGGATGGCGAAATTCGAGCCAGGCAAACTT
ACAAAATCAGGGCCTCAACCGATGAGTCTATCCCAAAAATTGTGCAAGCTGAGCGTCGGACGATTTTGAAGTCTCAGTAC
GCACCTGCAGATAATTGCGAATTAACCGCTAAATACATAGAGGCCACGGGGCAGAAGGTTGTGCGTGTGCAACCGTTTCAT
GTGCGACACACCTCCTGAAAAGGGTGGCCTGCCCCCTGGTAAACCTGGCATACCCATTTGGTACCTTGGTCAAGAATGA

>ORF16925 (SEQ ID NO:236)

AGGCCACGGGGCAGAAGGTTGTGCGTGTGCAACCGTTTCATGTGCGACACACCTCCTGAAAAGGGTGGCCTGCCCCCTGGT
AAACCTGGCATAACCATTTGGTACCTTGGTCAAGAATGATGTTTTTATGCCGCCCTGGGCTTTGACGCCGATTAAAGCAAA
GCTGTGTTTCGCTCATCAATACGTCCTCGCCAGTTAAACGACTGTTATGTATATGGGTGCTGCCGCTACGTAATACCT
TGGCCCTACGCATACGAAGTTAATTCGAAAGCGTTCAATGGACAATCTTCCTCCTCGGCGTCGACTGCAGCGGTAAGGT
GATCTACTTTTCGAAACACTGCAAGGGTAGGTCTTTTTTGGCAGCGTCCATATACCGACCGTGGTATGGCTCAGATGCGC
TGGTACTGCATTTACCAAATAA

Fig. 3-15

>ORF17793c (SEQ ID NO:238)

GCCAAAATGATTGTCATTGACAAAATCTAGAACATCTTGTGCGCAATGCGCTATATGTGAAAAAATTTATTTGACGA
GTTTTCTCTCAAGATTCAATTGGGGCATACATATTACGAGCCAAAATCTTTGCCCGCCTCTGCAAGCATTGTATATGGGT
CGCATCCAGCCCCGTCGACGTTTTTTTTTGGAACAAAAGAAATTCAGCAAAATTTGGTGCTGAAATCCGGTGAGCAAGTC
ATCACCTGCAGTAAACATCGATACAAAATACCGTTAGATTATTTGGTCTGGTGCAAACCAAAGGAACCCCTTGCGCGATT
GTTTCGTGCAGGTAACCTGTAATGACGGTCAGGTAGAGCCGGGGTTTCGACGGGTACGTAACCCCTTGAAATCGTCAATATGT
CGCCTTGGACGATAGAAATACCGGCCGTGAGCGATATAGCACAACTTTATTTGGTGAAATGCAGTACCAGCGCATCTGAG
CCATACCACGGTCGGTATATGGACGCTGCCAAAAAGGACCTACCCTTGAGTGTTTCGAAAGTAG

>ORF18548c (SEQ ID NO:240)

AGGACAATGGCAGGGTGGCCGCTCTCGCAGCCCAAGGACGAAGGACAAATCTGATGAGTGTGTTACAGATCAAAGGGCG
TACAACGAAATCCACACGGATTTTGACGGCGCATCGTACTCCAGCAACAGCCTTATACTACTGATGCAGGGGACGAGA
GAATTGAAGAGTTTTCCCTCGAATTGTCCGTGGGTGAAGGGTGGAGTGATAACTATTCTGGCAACGACAAAAACCTGTGG
CGCATTGTGATGGTATGACGATCAGGGGTACGATTCTGTTGTGGTGGAGGCCGCTGAAGAAATCAAGGTGCCGCACAA
TCGGTACGGCATAGTCTACCTACGGGAAGTCTTTTTCTCTCACGGCGTGTGTTGCTTCGGCGAAGGTGCAACCTG
CATTTGATGGCAAGCTCAAGCTCAGGATATTCAACACCACCAACAAAATGTCTGCCTTACCAAAGGCGAGAAGCTTGGC
TCTGTGATTTTTTTCTCCACAGAATCGACGCACACCCAAAGCCCCATCAAGCGTGGCAGTGAATATCGACGCTTCCCAT
CACGCGCGCGCGGATTGAAGAAGTGGTTTTTCGCTCAATCCACCATATGGGTGCGGTGGACGCTGAATTTAATCGGAA
GTTCCCTGGTGTCTTCTTATAATGTACGCCGTCTATTACAAGGTTGTGCTGGAAACACAGTCGACGCTCCTCAGTCA
CAACAAAACGCTCAGCCATCGCCGAACGAAGTTAAGCCAAAATGA

>ORF17875 (SEQ ID NO:242)

ACGGCGTACATTATAAGAGAAGACACCAGGGAACTTCCGATTAAATTCAGCGTCCACCCGACCCATATGGTGGGATTGAG
CGAAAACCACTTCTTCAATCGCGCGCGCGCGTGATGGGAAGCGTCGATATTTCACTGCCACGCTTGATGGGGCTTTGGG
TGTGCGTCGATTCTGTGGAGAAAAAATCACAGAGCCAAGCTTCTCGCCTTTGGTAAGGCAGACATTTTTGTTGGTGGTG
TTGAATATCCTGAGCTTGAGCTTGCCATCAAATGCAGGTTTCGACCTTCGCCGAAGCAACCAGCACGCCGCGTGAGAGAAA
AAGACTTCCCGTAGGTAGGACTATGCCGTACCGATTGTGCGGCACCTTGATTTCTTCAGCGGCCTCCACCACAACAGAAT
CGTGA

>ORF18479 (SEQ ID NO:244)

TCTGTAACACACTCATCAGATTGTCTTCTGCTCCTTGGGCTGCGAGACGCGGCCACCCTGCCATTGTCCTTTATACCGGC
CGATATCCCCGGATACCGCCTGAAAGATGACGTGCGCAAAGCGTGACCAATCTGAATTTCAAACGCCTCGCTGTGATTG
TTGGTGAGCGCGAACGTCATCGGCCCTACATAACCTGGAGGCAGCACACTGGAACCTGAACGTTATCCCGCTTCTGAACAG
CGTGCTTCTCGGAAAAAAGCGCGCCAGATCTCCGGCAGATCGAATTTCTTCATGGTGCTCGCCAGATAAGTCTTGC
CCGGTTCCATGACGAAGCAGTCATCCGGGTCTGCGAGCACGACCTCGCTGGCAGGGGTGCGTCGCGTAGATTCTCGCAAG
CTTCCACCCCTACTGTGAGGCGAGAGAGCCCTGCGAGTCTGAGGTCAAATCCAACGCCTTCCGGGGTGGTCAACTCACG
GTGGGCAAGGTGCTTGATTAG

>ORF19027c (SEQ ID NO:246)

ATGATTTACTCACCGCACTCGCTCCTGAAACTGGTCCGGGATGGAAAATAATCAAGCACCTTGCCACCGTGAGTTGAC
CACCCCGGAAGGCGTTGGATTTGACCTCAGACTCGCAGGCCTCTCTCGCCTGACAGTAGGGGGTGAAGCTTGCGAGAAT
CTACGCGACGCAACCCCTGCCAGCGAGGTCTGTGCTCGCAGACCCGGATGACTGCTTCGTATGGAACCGGGCAAGACTTAT
CTGGCGAGCACCATGGAAGAATTCGATCTGCCGGAAGATCTGGCGGCGCTTTTTTTTCCGAGAAGCACGCTGTTCAGAAG
CGGGATAACGTTCAAGTTCAGTGTGCTGCCTCCAGGTTATGTAGGGCCGATGACGTTTCGCGCTCACCAACAAATCACAGCG
AGGCGTTTGAATTCAGATTGGTGCACGCTTTGCGCACGTATCTTTTCAGGCGGTATCCGGGGATATCGCCCGGTATAAA
GGACAATGGCAGGGTGGCCGCGTCTCGCAGCCCAAGGACGAAGGACAAATCTGA

>ORF19305 (SEQ ID NO:248)

TGGCCGTTCTCTGCCTGTGCGCTCTTTGGCATGACTGGTCAAGTCGGATGCAAACGGTGGTCAGCACCAATGCAATTGGG
TGGTCATGTGCGATGCAATTACGCAATTGAGCCTGGCCAGTTCTTCCCAAGCAAAGCATAAGACCAAGATGGCACATTG
CCAACAAAATACCCCTCCCCGCTACCGTTGTTTTATCGTTGTTGCCAGCCCTGATCTGGCGGAAAAGCCCGCTCCATGAA
TCGTCATGGAGCCTCCCATGTTTCAACTCCTTTCTGGATATCCAGGAAGCCGTCCCCACCCCAACAACCAAGCTGCC
CCAGGGGGATTATCCTTCTCTGA

Fig. 3-16

>ORF19519 (SEQ ID NO:250)

TCTGGCGGAAAAGCCCGCTCCATGAATCGTCATGGAGCCTCCCATGTTTCAACTCCTTTCTGGATATCCAGGAAGCCGT
CCCCACCCCAACAACAAAGCTGCCCCAGGGGGATTATCCTTCCTCTGAGCAGCATGGAAGTCTCGGCACGCCTCGC
CGCCGGCAGCTACTGGAGAACATCTGGCAGCGCGCCTCGCTATCCAAGCAGCAATTCGAGGAGATCTACCGGCGGCCACT
GGCCAACTATGCCGAGCTGGTCCAGCAGCTCCCTGCTTCGGAAAATCATCACCATGCCCATCCAGGCGGGATGATCGATC
ACGGCCTGGAGATCGTGGCTACGCACTCAAGGTACGGCAGACCTACCTGCTCCCGATCGGCGCAGCGCCGGAGTCACAG
TCAGCCCAGGCTGA

>ORF19544 (SEQ ID NO:252)

ATCGTCATGGAGCCTCCCATGTTTCAACTCCTTTCTGGATATCCAGGAAGCCGTCCCCACCCCAACAACAAAGCTGC
CCCAGGGGGATTATCCTTCCTCTGAGCAGCATGGAAGTCTCGGCACGCCTCGCCGCGGCAGCTACTGGAGAACATCT
GGCAGCGCGCCTCGCTATCCAAGCAGCAATTCGAGGAGATCTACCGGCGGCCACTGGCCAACTATGCCGAGCTGGTCCAG
CAGCTCCCTGCTTCGGAAAATCATCACCATGCCCATCCAGGCGGGATGATCGATCAGGCGCTGGAGATCGTGGCCTACGC
ACTCAAGGTACGGCAGACCTACCTGCTCCCGATCGGCGCAGCGCCGGAGTCACAGTCAGCCCAGGCTGAAGCCTGGTCGG
CCGCGCGCGCTATGGCGCCCTGGCTCATGACATAGGCAAGATCGTCGTCGACCTGCAGGTTGAGCTACAGGACGGCAGC
ACCTGGCACCCTTGAACCGGACCGATCAACCAGCCATACCGCTTCAAGTACGTGAAGTCCCGCGAATACCAGCTCCACGG
CGCTGCCTCAGCACTTCTCATCCACCAACTGCTACCGCGCACTGCACTCGATTGGCTCAGTCGCTTTCCAGAGCTGTGGG
CTCAATTGATCTACCTGTTGCTGGGCACTACGAGCAGCGCGGGATCCTCGGCGAGATCATCGTGAAGGCAGACCAGGCC
TCAGTTGCACAGGAGCTAGGAGGCAATCCGGATCGAGCTCTGGCTGCACCGAAGCAGTCGCTGCAGCGGCAGTTGGCAGA
CGGCCTTCGCTTCTTGGTGAAGGACAAGTTCAAGTTGAATCAACCTAGCGGCCCGTCTGATGGATGGCTGACCCAGGACG
CACTCTGGCTGGTGAAGCAAGCCTGCTGCCGATCAACTGAGAGCCTACCTGCTGGCCAGGGTATCGATGGGGTGCCCTCC
TCTAACGCGCCGTTCTTTCAGCATGCTCCAGGACCAAGCCGTCATCCAGACAAATGCCGAGGACAAGGCCATTTGGACGGC
CACGGTAGACAACGGTGTGGATGGAGAAAACAAGTTACGCTACTCAAGATTGCTCCAGCCTTGATCTGGACAGATGCTG
CCGAGCGCCCTCACCTACAGCGGATCACTGGTCTTGAAGATGGAACCGCCTCAACGGAAGCCGGAACGACCTGT
GAAATTCCCAACGGGCGCGCTGAACAGCAGCAAGCACCAGAAACGAAGATGATGCTCCATCAACCTGCGCCGAGCGTTGC
GAAACCGGCAACGAGACGCGAGGCGATTGCGAAACCTCAACTGATGATCAAGAAGAAACAGACGATTTGTATGCACTTC
TTGGTAATATCAATTCCGCACTAGAAGAGCTAGACACTAGCCACGACTCGCCGGCTGCCTCTCCTACGAACACACGCGGG
GAGGAGAACCTACAGCAGCCACTAGGGACCAAGGAGCAACAGATTGCGCTCCTGAAGCAATTGAAGATGTATTTATGCC
TAGCAGAAGTACTGATCTGGGACAGGGATTCTGTTGGTGGATGAAATCTGGCATCGCGGCCGCTCGCCTGTTTATCAACG
ACACCAAGGCTTTGGTGCATACCGTAGACGGGACCGCCATGCTGGTCAAGCCAGGAATTTTCAAGCGCTATGTCCAAGAG
CATCCGGTGTGTTGAAAACTGGCCCAAGCAAGGAGACGACCGGCTGGAAGCTGGTGCAGCGCGGTTTCAAAAAACGGG
GCTTCATCGGAAGACCAGTAAAAACCTGAACATCTGGACCATCAAGGTTTCTGGTCTCGAAGACGAAAGAGCTCAAGG
CCTACCTGCTCCAGGATCCCAAATTGCTGTTCCCTGAGCAGCCTCTGGACAACCAAGCCTCACGGTCATCACCGATGCC
GAAGGAGGTGTGAATGA

>ORF20008 (SEQ ID NO:254)

GCTACAGGACGGCAGCACCTGGCACCCCTTGAACGGACCGATCAACCAGCCATACCGCTTCAAGTACGTGAAGTCCCGCG
AATACCAGTCCACGGCGCTGCCTCAGCACTTCTCATCCACCAACTGCTACCGCGCACTGCACTCGATTGGCTCAGTCGC
TTTCCAGAGCTGTGGGCTCAATTGATCTACCTGTTGCTGGGCACTACGAGCAGCGCGGGATCCTCGGCGAGATCATCGT
GAAGGCAGACCAGGCTCAGTTGCACAGGAGCTAGGAGGCAATCCGGATCGAGCTCTGGCTGCACCGAAGCAGTCGCTGC
AGCGGCAGTTGGCAGACGGCCTTCGCTTCTTGGTGAAGGACAAGTTCAAGTTGAATCAACCTAG

>ORF20623c (SEQ ID NO:256)

CGTGAACCTGTTTCTCCATCCAGCACCGTTGTCTACCGTGGCCGTCCAAATGGCCTTGCTCTCGGCATTTGTCTGGATGA
CGGCTTGGTCTGAGCATGCTGAAGAACGGCGCGTTAGAGGAGGGCACCCATCGATAACCTGGGCCAGCAGGTAGGCT
CTCAGTTGATCGGCAGCAGGCTTGTCAACAGCCAGAGTGCCTCTGGGTGAGCCATCCATCAGACGGGCGGCTAGGTTG
ATTCAACTTGAACCTTGCTTTCACCAAGAAGCGAAGGCCGTCTGCCAACTGCCGCTGCAGCGACTGCTTCGGTGCAGCCA
GAGCTCGATCCGGATTGCCTCCTAG

Fig. 3-17

>ORF21210c (SEQ ID NO:258)

CGCTTGAAAAATTCCTGGCGTGACCAGCATGGCGGTCCCGTCTACGGTATGCACCAAAGCCTTGGTGTGCTTGATGAACAG
GCGACGGGCGCGATGCCAGATTTTCATCCAACCAACGAATCCCTGTCCAGATCAGTACTTCTGCTAGGCATAAATACAT
CTTCAATTGCTTCAGGAGCGCAATCTGTTGGCTCCTTGGTCCCTAGTGGCTGCTGTAGGTTCTCCTCCCCGCGTGTGTTT
GTAGGAGAGGCGAGCCGGCGAGTCGTGGCTAGTGTCTAGCTCTTCTAGTGGCGAATTGATATTACCAAGAAGTGCATACAA
ATCGTCTGTTTCTTCTGA

>ORF21493c (SEQ ID NO:260)

GCTGCTGCGCGTCATTCCACACCTCCTTCGGCATCGGTGATGACCGTGAGGCTTGGGTTGTCCAGAGGCTGCTCAGGGA
ACAGCAATTTGGGATCCTGGAGCAGGTAGGCCCTTGAAGCTCTTTCGTCTTGCAGGAGACCAGAAACCTTGATGGTCCAGATG
TTCAGGTTTTTACTGGTCTTCCGATGAAGCCCCCTGTTTTTCGAACGCGCGCTGCACACAGCTTCCAGCCGGTCTGCTCCTT
GGCTTGGGCGAGTTTTTCAAGCACCGGATGCTCTTGGACATAGCGCTTGAATAATCCTGGCGTGACCAGCATGGCGGTCC
CGTCTACGGTATGCACCAAAGCCTTGGTGTGCTTGATGAACAGCGGACGGGCGCGATGCCAGATTTTCATCCAACCAACG
AATCCCTGTCCAGATCAGTACTTCTGCTAGGCATAAATACATCTTCAATTGCTTCAGGAGCGCAATCTGTTGGCTCCTT
GGTCCCTAG

>ORF21333 (SEQ ID NO:262)

ACATCTGGACCATCAAGTTTTCTGGTCTCGAAGACGAAAGAGCTCAAGGCCTACCTGCTCCAGGATCCCAAATTGCTG
TTCCCTGAGCAGCCTCTGGACAACCCAAGCCTCAGGTCATCACCGATGCCGAAGGAGGTGTGGAATGACGCCGCGAGCAG
CTCACCGAGGAGTACATCTTCGCGCACGATCTCCGGGAAGCCAGCGCGAAGATCTACCGCGCCGCGACCAAGGCGCTGCT
CAAGCACTTCGGTCTACGGCAACCGTACAGGACCTGGACCACCGGGCTGTCTGGGATGGCGACGCAAGGTAAGTGAAC
AAGGCCTGTCCAAGCGGAGCTGGAACACGTACTCGAATCATCTGCGGACGATCTGGGGCTATGCCATCGAGCATGA

>ORF22074c (SEQ ID NO:264)

GTGAGGCACAAGCCCCCTCCGTTATTGGCACTACGAACTCTTTGTGAGTCTTCTGTCTCGCCGCGGATGAGGATCAGTT
GATTTTCCAGTCGATGTCCGCTTTCGGATGCACAACAGCGCATTCAACCGGATGCCGGTGAAGTAGAAGACCTCAAAC
GTGCAAAGCCAGAACCAGGCGGGCGTGATCCGTGCGCGTTTCGCCGGTGCAGCGCTCTGCGCGCTCTGTCATGTTGAGCCA
ATTGCGGGCGAGCAGGATGGCTTCGGCGGCGACGTTTTGTCTGCTCGCCTGGGGGAATGACGGTGGTCTTTCTGAACG
GGTTGACTTGGGAGTGCCTCACCACTCATGCTCGATGGCATGCCCCAGATCGTCCGACGATGATTCGAGTACGTGTTT
CAGCTCCGTTGGACAGGCCTTGTTCAGTACCTTGTGCTCGCCATCCAGGACAGCCCGGTGGTCCACGCTCTGTACGGT
TGCCGTAGGACCGAAGTGCTTGGACAGCGCCTTGTGCGGGCGCGGTAGATCTTCGCGCTGGCTTCCCGGAGATCGTGGC
CGAAGATGTACTCTCGGTGAGCTGTGCGGCGTCATTCCACACCTCCTTCGGCATCGGTGATGACCGTGAGGCTTGGGT
TGTCCAGAGGCTGCTCAGGGAACAGCAATTTGGGATCCTGGAGCAGGTAG

>ORF21421 (SEQ ID NO:266)

GCAGCCTCTGGACAACCAAGCCTCACGGTCATCACCGATGCCGAAGGAGGTGTGGAATGACGCCGCGAGCAGCTCACCGA
GGAGTACATCTTCGCGACGATCTCCGGGAAGCCAGCGCGAAGATCTACCGCGCCGCGACCAAGGCGCTGCTCAAGCACT
TCGGTCTACGGCAACCGTACAGGACGTGGACCACGGGCTGTCTGGGATGGCGACGCAAGGTAAGTGAACAAGGCCTG
TCCAAGCGGAGCTGGAACACGTACTCGAATCATCTGCGGACGATCTGGGGCTATGCCATCGAGCATGAGTTGGTGACGCA
CTCCCAAGTCAACCCGTTCAAGAAAGACCACCGTCATTCCCCCAGGCGAGCAAGCAAAACCGTCGCCGCGGAAGCCATCC
TGCTCGCCCCCAATTGGCTCAACATGCAGGACGGCGCAGAGCGCTGCACCGGCGAAGCGCGACGGATCACGCCCCGCTGG
TTCTGGCTTTGCACGTTTGAGGTCTTCTACTTCACCGGCATCCGGTTGAATGCGCTGTTGTGCATCCGCAAGCGCGACAT
CGACTGGGAAAAATCAACTGATCCTCATCCGCGCGGAGACAGAGAAGACTCACAAAGAGTTCTAGTGCCAAATAACGGAGG
GGCTTGTGCTCACCTATCGAGGCTCCTGCAAGAGGCGGATAGAGCCGGATTCGCCGATGACGACCAAGTTGTTCAACGTC
AACCGGTTCTCACCGCACTACAAGAGCAAGGTGATGAACTCCGACCAGGTGCAAGCCATGTACCGGAAGTTGACCGAGAA
GGTTGGGGTGCGGATGACCCCGCACCGTTTCCGGCACACCTGGCCACCGACTTGATGAAGGCAACCGAGCGGAACATTC
ACCTCACGAAGTGCCTGCTCAACCACTCGAATATCCAGACCAGATGAGCTACATCGAGGCCGACTACGATCACATGCGT
GCCGTGCTGCATGCTAGAAGCCTGGCCCAAGGCGCGCTGGAGAATGTGAGGAAGGTGGATTACAGCGGCTCCCCGCAAGC
CTCTGCCAAACCGAAGCCATGCGGGCAACCTCTCGCTCGAGTGAGTGAAGCGCGCCACCGGAGGCCAGGACAGAGCCTG
CAGAACCAAGGGAGCACAGCCAGGGACAGGCATTAGGGAGGTCCAACCGCTGGGAAGCAGATGCGCTACACAGCCA
CCTGACACCTTCGAACCAAGCGTGTGTTCACTCTGATGGCTCAAACTTATCGAACCCTGCCGCTCGGCATCCGCGGC
TCCCGCTGCAACAAGCGGATCAGGCGGATGGGGATCTGCCGCCCGAAGCAATCTCGCCTAG

Fig. 3-18

>ORF22074c (SEQ ID NO:264)

GTGAGGCACAAGCCCCTCCGTTATTGGCACTACGAACTCTTTGTGAGTCTTCTGTCTCGCCGCGGATGAGGATCAGTT
GATTTTCCAGTCGATGTCGCGCTTGCGGATGCACAACAGCGCATTCAACCGGATGCCGGTGAAGTAGAAGACCTCAAAC
GTGCAAAGCCAGAACCAGGCGGGCGTGATCCGTGCGCGTTTCGCCGGTGCAGCGCTCTGCGCCGTCCTGCATGTTGAGCCA
ATTGCGGGCGAGCAGGATGGCTTCGGCGGCGACGGTTTTGCTTGCTCGCCTGGGGGAATGACGGTGGTCTTTCTGAACG
GGTTGACTTGGGAGTGCGTCACCAACTCATGCTCGATGGCATAGCCCCAGATCGTCCGCAGATGATTCGAGTACGTGTTT
CAGCTCCGCTTGGACAGGCCTTGTTCCAGTACCTTGCGTCGCCATCCCAGGACAGCCCGGTGGTCCACGTCTGTACGGT
TGCCGTAGGACCGAAGTGCTTGAGCAGCGCCTTGCTGCGGGCGCGGTAGATCTTCGCGCTGGCTTCCCGGAGATCGTGCG
CGAAGATGTACTCCTCGGTGAGCTGCTGCGGCGTCATTCCACACCTCCTTCGGCATCGGTGATGACCGTGAGGCTTGGGT
TGTCCAGAGGCTGCTCAGGGAACAGCAATTTGGGATCCTGGAGCAGGTAG

>ORF21421 (SEQ ID NO:266)

GCAGCCTCTGGACAACCCAAGCCTCACGGTCATCACCGATGCCGAAGGAGGTGTGGAATGACGCCGCGAGCAGCTCACCGA
GGAGTACATCTTCGCGCACGATCTCCGGGAAGCCAGCGCGAAGATCTACCGCGCCGCGACCAAGGCGCTGCTCAAGCACT
TCGGTCTACGGCAACCGTACAGGACGTGGACCACCGGGCTGTCTGGGATGGCGACGCAAGGTACTGGAACAAGGCCTG
TCCAAGCGGAGCTGGAACACGTACTCGAATCATCTGCGGACGATCTGGGGCTATGCCATCGAGCATGAGTTGGTGACGCA
CTCCCAAGTCAACCCGTTTCAGAAAGACCACCGTCATTCCCCCAGGCGAGCAAGCAAAACCGTCGCCGCCGAAGCCATCC
TGCTCGCCCGCAATTGGCTCAACATGCAGGACGGCGCAGAGCGCTGCACCGGCGAACGCGCACGGATCACGCCCCGCTGG
TTCTGGCTTTGACGTTTGAGGTCTTCTACTTCACCGGCATCCGGTTGAATGCGCTGTTGTGCATCCGCAAGCGCGACAT
CGACTGGGAAAATCAACTGATCCTCATCCGCGGCGAGACAGAGAAGACTCACAAAGAGTTTCGTAGTGCCAAATAACGGAGG
GGCTTGTCCTCACCTATCGAGGCTCCTGCAAGAGGCCGATAGAGCCGGATTTCGCCGATGACGACCAGTTGTTCAACGTC
AACCGGTTCTCACCGCACTACAAGAGCAAGGTGATGAACTCCGACAGGTGCAAGCCATGTACCGGAAGTTGACCGAGAA
GGTTGGGGTGCGGATGACCCCGCACCGTTTTCCGGCACACCCCTGGCCACCGACTTGATGAAGGCACCCGAGCGGAACATTC
ACCTCACGAAGTGCTGCTCAACCACTCGAATATCCAGACCAGTACGCTACATCGAGGCCGACTACGATCACATGCGT
GCCGTGCTGCATGCTAGAAGCCTGGCCCCAAGGCGCGCTGGAGAATGTAGGAAGGTGGATTACAGCGGCTCCCCGAAAGC
CTCTGCCAAACCGAAGCCATGCGGGCAACCTCTCGCTCGAGTGAGTGAAGCGCCGCCACCGGAGGCCAGGACAGAGCCTG
CAGAACCAAGGGAGCACACGCCAGGGACAGGCATTAGGGAGGTCCAACCGCGTGGGAAGCAGATGCGCTACCACAGCCA
CCTGACACCTTCGAACCAAGCGTGCTGTTCACTCTGATGGCTCAAACTTATCGAACCGTGCCGCTCGGCATCCGCGGC
TCCCCTGCAACAAGCGGATCAGGCGGATGGGGATCTGCCGCCGAAGCAATCTCGCCTAG

>ORF22608c (SEQ ID NO:268)

CGCATCTGCTTCCACGCGGTTGGACCTCCCTGAATGCCTGTCCCTGGCGTGCTCCCTTGGTTCTGCAGGCTCTGTCC
TGGCCTCCGGTGGCGGCTTCACTCACTCGAGCGAGAGGTTGCCCGCATGGCTTCGGTTTGGCAGAGGCTTGCGGGGAG
CCGCTGTAATCCACCTTCTGACATTCTCCAGCGCGCTTGGGCCAGGCTTCTAGCATGCAGCACGGCACGCATGTGATC
GTAGTCGGCCTCGATGTAGCTCATCGTGGTCTGGATATTCGAGTGGTTGAGCAGGCACTTCGTGAGGTGAATGTTCCGCT
CGGGTGCTTTCATCAAGTCGGTGGCCAGGGTGTGCCGGAACGGTGGGGGTTCATCCGCACCCCAACCTTCTCGGTCAAC
TTCCGGTACATGGCTTCGACCTGGTTCGGAGTTCATCACCTTGCTCTTGTAGTGCGGTGA

>ORF22626 (SEQ ID NO:270)

CACCTTCGAACCAAGCGTGCTGTTCACTCTGATGGCTCAAACTTATCGAACCGTGCCGCCTCGGCATCCGCGGCTCCCG
CTGCAACAAGCGGATCAGGCGGATGGGGATCTGCCGCCCGAAGCAATCTCGCCTAGCGATACCGGTACTGAGGGCCGGCT
ACCGGACGAAAGGTAGCCGTGCCTTCCAGCAGATCGTTAGGCCTGTAGGAAAAATCTGGAATTACCGAGAGCGCCTGGAT
TCCAGCGCCGGCATGCTGGCAGAGCCAGCGCAATTTCAAGGCCAATACCACAGTACCCTCTGTAATCGCTGA

Fig. 3-19

>ORF23228 (SEQ ID NO:272)

AGAGATTGAACTCCCGACATCCTGCTCCCAAAGCAGGCGCGCTACCGGACTGCGCTATACCCCGATTGGAATTTGGCTC
CGCGACCTGGACTCGAACCAGGGACCCAATGATTAAACAGTCATTTGCTCTACCGACTGAGCTATCGCGGAACGCTTTCT
TCCAACCCCTGGACGCTTCCGGTGTTGCTGGATTGCGCTCTCAGAGGCGCGCCATTTTACGGATGCGCGGGGCATGTCAA
CCCTCTGATCCAAAAGTTTTCTTCTTTTCCACGAGCGACAAAACGGCCCTTCCACTGCATGCGGCAGCGCTCTCGCG
CCTACCGGACGCCCCATGAAAAAGCCCCGCCGAAGCGGGGCTTCCCTGTCCGCCCCGAAGAGGTGAGGCGAAGACGATC
TCGTGCGCTTCCACCTTCGCCGAGATACTGGCACCCGGCGCAATTTGCCGGCCAGGATCAGTTGCGCCAGCGGGTTCTC
GATCCAGCGCTGGATGGCCCCGCTTCAGCGGGCGTGCGCCATAGACGGGTGGAAGCCGACGGCAATCAGCTTGTCCAGCG
CCTCCTGGCTCAGTTCCAGGCTCAGCTCGCGCTCGGCCAGGCGCTTGCAGGCGACCGAGCTGGATCTCGGCGATGCCG
GCGATCTGCTCGCGAGCCAGCGGCTCGAACACCACCACTTCGTGATCCGGTTGATGAATTCGGGACGGAAGTGCGCATT
GACCGCGTCCATCACTGCGGCACGTTGCGCCTCGCGGTGCGCGGCCAGCTCCTGGATCTGCGCCGAACCGAGGTTGGAGG
TCATCACCACCGGTGTTGCGGAAGTCCACCTACGCCCCGTGACTGTGCGTCAGGCGTCCGTCTCGAGCACCTGGAGG
AGAATGTTGAATACATCCGGATGGGCCTTCTCCACCTCGTCCAGCAGCACCACCGAGTAGGGCTTGCGGCGGATCGCCTC
GGTCAGGTAGCCGCTTCTCGAAGCCGACGTAGCCCCGAGGCGCGCCGATCAGGCGGGCCACCGAGTGTCTTCTCCATGA
ACTCGGACATATCTATCCGCACCAGCGCCTCCTCGGTATCGAAGAGGAACTCGGCCAGCGCCTTGACAACTCGGTCTTG
CCCACCCCGTTCGGGCCGAGGAAGAGGAACGAGCCGCTCGGCCGGTTCCGATCGGCGAGGCGGCGCGCAACGGCGCAC
GGCGTTGGACACGGCGACTACCGCCTCGTCTGGCCGATCACTCGCCGATGCAGCTCCTGCTCCATGCGCAGCAGCTTCT
CGCGCTCGCCCTCGAGCATCTTCGACACCGGGATACCGGTCCACTTGGAACCACTTCGGCGATTTCTCGTGGTCAAC
TTGTTGCGCAGCAACTGGTTCTCGGTCTTGGCGTCTGGTGCACCATCTGCAGGCTGCGTTCCAGGTCCGGGATGGTCTG
GTACTGGATGCGCGCATGCTCTCAGAGTGCCTTGGCGCGCGCCGCTCCATCTCCTGCTTGGCCTGCTCGATCTTCT
GCTGGATCTGCGCGAGCCCTGCACCTCGGCCCTTCTCGGACTTCCAGATCTCCTCGAGGTGCGGCTATTGCGCTCGAGC
TTGACGATATCCTCCTCCAGCTTGGCCAGGCGCTTCTGGTGGCTTCGTGCTCTTCTTCTCAGCGCTCGCGCTCGAT
CTTCAGCTGGATCAGGCGACGGTCGAGACGATCCAGTTCTCCTCGGCTTGGAGTCGATCTCCATGCGGATGCGGCTGGCGG
CCTCGTCGATCAGGTGATGGCCTTGTCCGGCAGTTGCCGATCGGTGATGTAGCGGTGCGACAGCTTGGCCGCGGCGATG
ATCGCGCCGTGCGTGATGCTACCCCGTGGTGCATTCATAGCGTTCTTGAGGCCACGGAGGATGGCGATGGTGTCTTC
CTCGCTCGGTTCTCCACCAGCACCTTCTGGAAGCGCGCTCCAGCGCGGCATCTTCTCGATGTACTGGCGATACTCGT
CGAGGGTAGTAGCACCGACGCACTGCAGCTCGCCGCGCGCCAGAGCCGCTTGAAGATGTTGCCGGCTCCATGGCACCT
TCCGCTTGGCCGCGCCGACCATGGTGTGAGTTCGTGATGAACAGGATGACCCGGCTTCTGCTTGGCCAGTTCTGTT
GAGGACCGCTTCAAGCGTTCTCGAACTCGCCGCGGAACCTGGCACCGGCGATCAGCGCCCCATGTCCAGGGCCAGCA
GGCGCTTGTCTTGAAGCGCTCCGGCACTTCGCCGTTGATGATGCGCTGGGCCAGGCCCTCGACGATGGCGGTCTTGCCG
ACGCCGGTTTCGCCGATCAGCACCGGGTGTCTTGGTCCGCCGCTGCAGGACCTGGATGGTCCGGCGGATCTCGTCTGTC
GCGACCGATACCCGGGTGAGCTTGCCTTCTCGCGCGCTTGGTCATGTGACGGTGTACTTGTCCAGCGCTTGGCGCG
ACTCCTCGACGTTCCGGTCTTACCGCTTCCGCCGACGAGGTTGGCCACGGCATTCTCCAGCGCTTGGCGGACAGC
CCCTGGCCGAGCAGCAGCTTGGCGAGCCTGGTGTCTCGTCCATCGCGGCCAGCAATACCAGCTCGTGGAGATGAAGT
GTCGCCCTTCTGCTGGGCCAGGCGGTGAGCCTGGTTGAGCAGGCGTGCAGATCTGGGACAGGTTACGTCGCCGGTTCG
GGCTCTGGATCTTCGGCAGCGCTGAGTTCTTTGTTGAGGCGCTGCGCAGGGCGGCGATATCGAAGCCGACCTGCATC
AGCAGGGGCTTGATCGAACCGCTTGTGCTCGAGCAGGGCGGAAGCAGGTGCACCGGCTCGATGGCCGGATGGTCATG
GCCAACGGCCAGGGACTGGGCGTGGAGAGCGCCAGTTGCAGCTTGTGGTCAAACGGTCTATTGCGATGGGTGCTCCTT
CCTTCTATAG

>ORF23367 (SEQ ID NO:274)

GCTATCGCGGAACGCTTTTCTTCCAACCTGGACGCTTCCGGTGTTGCTGGATTGCGCTCTCAGAGGCGCGCCATTTTAC
GGATGCGCGCGGGCATGTCAACCTCTGATCCAAAAGTTTTCTTCTTTTCCACGAGCGACAAAACGGCCCTTCCACT
GCATGCGGCAGCGCTCTCGCGCTACCGGACGCCCATGAAAAAGCCCCCGGAAGCGGGGCTTCCCTGTCCGCCCCGA
AGAGGTGAGGCGAAGACGATCTCGTCGCTTCCACCTTCGCCGAGATACTGGCACCCGGCGCAATTTGCCGGCCAGGAT
CAGTTGCGCCAGCGGTTCTCGATCCAGCGCTGGATGGCCGCTTACGCGGCGTGCGCCATAG

Fig. 3-20

>ORF25103c (SEQ ID NO:276)

AGTGCACCACGGGGTGAGCATCACCGACGGCGCGATCATCGCCGCGGCCAAGCTGTCGCACCGCTACATCACCGATCGGC
AACTGCCGGACAAGGCCATCGACCTGATCGACGAGGCCGCCAGCCGCATCCGCATGGAGATCGACTCCAAGCCGGAGGAA
CTGGATCGTCTCGACCGTCGCTGATCCAGCTGAAGATCGAGCGCGAGGCGCTGAAGAAGGAAGACGACGAAGCCACCAG
GAAGCGCCTGGCCAAGCTGGAGGAGGATATCGTCAAGCTCGAGCGCGAATACGCCGACCTCGAGGAGATCTGGAAGTCCG
AGAAGGCCGAGGTGCAGGGCTCGGCGCAGATCCAGCAGAAGATCGAGCAGGCCAAGCAGGAGATGGAGGCGGCGGCGC
AAGGGCGACCTCGAGAGCATGGCGCGCATCCAGTACCAGACCATCCCGGACCTGGAACGCAGCCTGCAGATGGTCGACCA
GCACGGCAAGACCGAGAACCAGTTGCTGCGCAACAAGGTGACCGACGAGGAAATCGCCGAAGTGGTTTCCAAGTGGACCG
GTATCCCGGTGTGCAAGATGCTCGAGGGCGAGCGCGAGAAGCTGCTGCGCATGGAGCAGGAGCTGCATCGGCGAGTGATC
GGCCAGGACGAGGCGGTAGTCGCCGTGTCCAACGCCGTGCGCCGTTTCGCGCGCCGGCCTCGCCGATCCGAACCGGCCGAG
CGGCTCGTTCCTTCTTCTCGGCCCGACCGGGTGGCAAGACCGAGTTGTGCAAGGCGCTGGCCGAGTTCTCTTCGATA
CCGAGGAGGCGCTGGTGCGGATAGATATGTCCGAGTTCATGGAGAAACACTCGGTGGCCCGCCTGATCGGCGCGCCTCCG
GGCTACGTCGGCTTCGAGGAAGCGGCTACCTGACCGAGGCGATCCGCCGCAAGCCCTACTCGGTGGTGCTGCTGGACGA
GGTGGAGAAGGCCCCATCCGGATGTATTCAACATTCTCCTCCAGGTGCTCGAGGACGGACGCCTGACCGACAGTCACGGGC
GTACGGTGGACTTCCGCAACACCGTGGTGGTGATGACCTCAACCTCGGTTCCGGCGCAGATCCAGGAGCTGGCCGGCGAC
CGCGAGGCGCAACGTGCCGAGTGATGGACGCGGTCAATGCGCACTTCCGTCCGGAATTCATCAACCGGATCGACGAAGT
GGTGGTGTTCGAGCCGCTGGCTCGCGAGCAGATCGCCGGCATCGCCGAGATCCAGCTCGGTGCGCTGCGCAAGCGCCTGG
CCGAGCGCGAGCTGAGCCTGGAAGTGAAGCAGGAGGCGCTGGACAAGCTGATTGCCGTGGGCTTCGACCCGGTCTATGGC
GCACGCCCCGTGAAGCGGGCCATCCAGCGCTGGATCGAGAACCCTGCTGGCGCAACTGATCCTGGCCGGCAAATTCGCGCC
GGGTGCCAGTATCTCGGCGAAGGTGGAAGGCGACGAGATCGTCTTCGCCTGACCTCTTCGGGGGCGGACAGGGAAAGCCC
CGCTTCGGCGGGGCTTTTTTCATGGGCGTCCGGTAGGCGCGAGAGCGCTGCCGCATGCAGTGGAAGGGCCGTTTTGTGCGT
CGTGAAAAAAGAAGAAAACTTTTTGGATCAGAGGGTTGACATGCCCGCGCGCATCCGTAAATGGCGCGCCTCTGA

>ORF23556 (SEQ ID NO:278)

AAAAGCCCCGCCGAAGCGGGGCTTTCCCTGTCCGCCCCGAAGAGGTCAGGCGAAGACGATCTCGTCGCCTTCCACCTTC
GCCGAGATACTGGCACCCGGCGCGAATTTGCCGGCCAGGATCAGTTGCGCCAGCGGGTTCTCGATCCAGCGCTGGATGGC
CCGCTTCAGCGGGCGTGCGCCATAGACCGGGTGAAGCCGACGGCAATCAGCTTGTCCAGCGCCTCCTGGCTCAGTTCCA
GGCTCAGCTCGCGCTCGGCCAGGCGCTTGGCGAGGCGACCGAGCTGGATCTCGGCGATGCCGGCGATCTGCTCGCGAGCC
AGCGGCTCGAACACCACCACTTCGTCGATCCGGTTGA

Fig. 3-21

>ORF26191c (SEQ ID NO:280)

AAGGAAGGACGACCCATGCGAATAGACCGTTTGACCAGCAAGCTGCAACTGGCGCTCTCCGACGCCCAGTCCCTGGCCGT
TGGCCATGACCATCCGGCCATCGAGCCGGTGCACCTGCTTTCCGCCCTGCTCGAGCAGCAAGGCGGTTTCGATCAAGCCCC
TGCTGATGCAGGTCGGCTTCGATATCGCCGCCCTGCGCAGCGGCTCAACAAAGAACTCGACGCGCTGCCGAAGATCCAG
AGCCCGACCGGCGACGTGAACCTGTCCAGGATCTCGCAGCGCTGCTCAACCAGGCTGACCGCTGGCCAGCAGAAGGG
CGACCAAGTTCATCTCCAGCGAGCTGGTATTGCTGGCCGCGATGGACGAGAACACCAGGCTCGGCAAGCTGCTGCTCGGCC
AGGGCGTGTGCGCAAGGCGCTGGAGAATGCCGTGGCCAACTGCGTGGCGGCGAAGCGGTGAACGACCCGAACGTCGAG
GAGTCGCGCCAGGCGCTGGACAAGTACACCGTCGACATGACCAAGCGCGCCGAGGAAGGCAAGCTCGACCCGGTGATCGG
TCGCGACGACGAGATCCGCCGGACCATCCAGGTCTGCGAGCGCGGACCAAGAAACAACCCGGTGCTGATCGGCGAACC
GCGTCGGAAGACCGCCATCGTCGAGGGCTGGCCAGCGCATCATCAACGGCGAAGTCCGGACGCGCTCAAGGACAAG
CGCTGCTGGCCCTGGACATGGGGGCGCTGATCGCGGTGCCAAGTTCGCGGCGAGTTCGAGGAACGCTGAAGGCGGT
CCTCAACGAACCTGGGCAAGCAGGAAGGCCGGGTGATCCTGTTTCATCGACGAACGACACCATGGTTCGGCGCCGCAAGG
CGGAAGGTGCCATGGACGCCGGCAACATGCTCAAGCCGGCTCTGGCGCGCGGAGCTGCACTGCGTGGTGCTACTACC
CTCGACGAGTATCGCCAGTACATCGAGAAGGATGCCGCGTGGAGCGCGCTTCAGAGGTGCTGGTGGACGAACCGAG
CGAGGAAGACACCATCGCCATCTCCTGGGCTCAAGGAACGCTATGAAGTGCACCATGGTTCGGCGCCGCAAGG
CGATCATCGCCGCGGCAAGCTGTGCGACCGCTACATCACCAGTCGGCAACTGCCGGACAAGGCCATCGACCTGATCGAC
GAGGCGCGCAGCGCATCCGCATGGAGATCGACTCAAGCGCGAGGAACCTGGATCGTCTCGACCGTTCGCTGATCCAGCT
GAAGATCGAGCGGAGGCGCTGAAGAAGGAAGACGACGAAGCCACCAGGAAGCGCCTGGCCAAGCTGGAGGAGGATATCG
TCAAGTTCGAGCGCAATACGCCGACCTCGAGGAGATCTGGAAGTCCGAGAAGGCGGAGTGCAGGGCTCGGCGCAGATC
CAGCAGAAGATCGAGCAGGCCAAGCAGGAGATGGAGGCGCGCGCGCAAGGGCGACCTCGAGAGCATGGCGCGCATCCA
GTACCAGACCATCCCGGACCTGGAACGCGAGCTGCAGATGGTCGACGACGCGCAAGACCGAGAACCAGTTGCTGCGCA
ACAAGGTGACCGACGAGGAAATCGCCGAAGTGGTTTCAAGTGGACCGGTATCCCGGTGTCGAAGATGCTCGAGGGCGAG
CGCGAGAAGCTGCTGCGCATGGAGCAGGAGCTGCATCGGCGAGTGATCGGCCAGGACGAGGCGGTAGTCGCGCTGTCCAA
CGCCGTGCGCGTTCGCGCGCCGGCTCGCCGATCCGAACCGGCGGAGCGGCTCGTTCCTCTTCTCGGCCCGACCGGG
TGGGCAAGACCGAGTTGTGCAAGGCGCTGGCCGAGTTCCTCTTCGATACCGAGGAGGCGCTGGTGGGATAGATATGTCC
GAGTTCATGGAGAAACACTCGGTGGCCCGCTGATCGGCGCGCTCCGGGCTACGTGCGCTTCGAGGAAGGCGGCTACCT
GACCGAGGCGATCCGCCGAAGCCCTACTCGGTGGTGTCTGCTGGACGAGGTGGAGAAGGCCCATCCGGATGTATTCAACA
TTCTCTCCAGGTGCTCGAGGACGAGCGCTGACCGACAGTCACGGGCGTACGGTGGACTTCGCAACACCGTGGTGGTG
ATGACCTCCAACCTCGGTTTCGGCGCAGATCCAGGAGCTGGCCGGCGACCGCGAGGCGCAACGTGCCGAGTGATGGACGC
GGTCAATGCGCACTTCGTCGGAATTCATCAACCGGATCGACGAAGTGGTGGTTCGAGCGGCTGGCTCGCGAGCAGA
TCGCCGGCATCGCCGAGATCCAGCTCGGTGCGCTCGCAAGCGCTGGCCGAGCGGAGCTGAGCCTGGAACCTGAGCCAG
GAGGCGCTGGACAAGCTGATTGCGCTCGGCTTCGACCCGGTCTATGGCGCAGCCCGCTGAAGCGGGCCATCCAGCGCTG
GATCGAGAACCCGCTGGCGCAACTGATCCTGGCCGGCAAATTCGCGCCGGGTGCCAGTATCTCGGCGAAGGTGGAAGGCC
ACGAGATCGTCTTCGCCTGA

>ORF23751 (SEQ ID NO:282)

ACCGGGTTCGAAGCCGACGGCAATCAGCTTGTCCAGCGCTCCTGGCTCAGTTCCAGGCTCAGCTCGCGCTCGGCCAGGCG
CTTGCGCAGGCGACCGAGCTGGATCTCGCGATGCCGGCATCTGCTCGCGAGCCAGCGGCTCGAACACCACCACTTCGT
CGATCCGGTTGATGAATTCCGGACGGAAGTGGCATTCACCGCGTCCATCACTGCGGCACGTTGCGCTCGCGGTGCGCG
GCCAGCTCCTGGATCTGCGCCGAACCGAGGTTGGAGGTATCACCACCAGGTGTTGCGGAAGTCCACCGTACGCCCGTG
A

>ORF24222 (SEQ ID NO:284)

CCCGGAGGCGCGCGATCAGGCGGGCCACCGAGTGTTCCTCATGAACTCGGACATATCTATCCGCACCAGCGCTCCTC
GGTATCGAAGAGGAACTCGGCCAGCGCTTGCACAACTCGGTCTTGCCACCCCGGTGGGCGGAGGAAGAGGAACGAGC
CGCTCGGCGGGTTTCGGATCGGCGAGGCGCGCGCAACGGCGCAGCGGCTTGGACACGGCGACTACCGCCTCGTCTGG
CCGATCACTCGCCGATGCAGCTCCTGCTCCATGCGCAGCAGCTTCTCGCGCTCGCCCTCGAGCATCTTCGACACCGGGAT
ACCGGTCCACTTGGAAACCACTTCGGCGATTTCCTCGTCGGTCACCTTGTGCGCAGCAACTGGTTCCTGGTCTTGCCGT
GCTGGTCGACCATCTGCAGGCTGCGTTCAGGTCCGGGATGGTCTGGTACTGGATGCGCGCCATGCTCTCGAGGTGCCCC
TTGCGCCGCGCCGCTCCATCTCCTGCTTGGCTGCTCGATCTTCTGCTGGATCTGCGCCGAGCCCTGCACCTCGGCCTT
CTCGGACTTCAGATCTCCTCGAGGTGCGGCTATTCGCGCTCGAGCTTGACGATATCTCCTCCAGCTTGCCAGGCGCT
TCCTGGTGGCTTCGTGCTTCTTCTTCAGCGCTCGCGCTCGATCTTCAGCTGGATCAGGCGACGGTCGAGACGATCC
AGTTCCTCGGCTTGAGTTCGATCTCCATGCGGATGCGGCTGGCGGCTCGTCGATCAGGTGATGGCTTGTCCGGCAG
TTGCCGATCGGTGATGTAG

Fig. 3-22

>ORF24368 (SEQ ID NO:286)

ACTCGGACATATCTATCCGCACCGCGCTCCTCGGTATCGAAGAGGAACTCGGCCAGCGCTTGCACAACTCGGTCTTG
CCACCCCGGTTCGGGCGGAGGAAGAGGAACGAGCCGCTCGGCCGGTTCCGATCGGCGAGGCCGGCGCGAAGCGCGCAC
GGCGTTGGACACGGCGACTACCGCCTCGTCTGGCCGATCACTCGCCGATGCAGCTCCTGCTCCATGCGCAGCAGCTTCT
CGCGCTCGCCCTCGAGCATCTTCGACACCGGGATACCGGTCCACTTGGAAAACCACTTCGGCGATTTCCTCGTCGGTCACC
TTGTTGCGCAGCAACTGGTTCTCGGTCTTGGCTGCTGGTCGACCATCTGCAGGCTCGGTTCCAGGTCCGGGATGGTCTG
GTACTGGATGCGCGCCATGCTCTCGAGGTGCGCCTTGGCGCGCGCCCTCCATCTCCTGCTTGGCTGCTCGATCTTCT
GCTGGATCTGCGCCGAGCCCTGCACCTCGGCCTTCTCGGACTTCAGATCTCCTCGAGGTGCGCGTATTGCGCTCGAGC
TTGA

>ORF24888c (SEQ ID NO:288)

AGAAGGAAGACGACGAAGCCACCGGAAGCGCTGGCCAAGCTGGAGGAGGATATCGTCAAGCTCGAGCGGAATACGCC
GACCTCGAGGAGATCTGGAAGTCCGAGAAGGCCGAGGTGCAGGGCTCGGCGCAGATCCAGCAGAAGATCGAGCAGGCCAA
GCAGGAGATGGAGGCGGCGCGCGCAAGGGCGACCTCGAGAGCATGGCGCGCATCCAGTACCAGACCATCCCGGACCTGG
AACCGAGCCTGCAGATGGTCGACCAGCACGGCAAGACCGAGAACCAGTTGCTGCGCAACAAGGTGA

>ORF25398c (SEQ ID NO:290)

AGGCGGTCTCAACGAACCTGGGCAAGCAGGAAGGCCGGGTTCATCCTGTTTCATCGACGAACCTGCACACCATGGTCGGCGCC
GGCAAGCGGAAGGTGCCATGGACGCCGGCAACATGCTCAAGCCGGCTCTGGCGCGCGGCGAGCTGCACTGCGTCGGTGC
TACTACCTTCGACGAGTATCGCCAGTACATCGAGAAGGATGCCGCGCTGGAGCGCCGCTTCCAGAAGGTGCTGGTGGACG
AACCGAGCGAGGAAGACACCATCGCCATCCTCCGTGGCCTCAAGGAACGCTATGAAGTGCACCACGGGGTGA

>ORF25892c (SEQ ID NO:292)

CCGCTGGCCAGCAGAAGGGCGACCAAGTTCATCTCCAGCGAGCTGGTATTGCTGGCCGCGATGGACGAGAACACCAGGC
TCGGCAAGCTGCTGCTCGGCCAGGGCGTGTGCGCAAGGCCGTGGAGAATGCCGTGGCCAACCTGCGTGGCGGCGAAGCG
GTGAACGACCCGAACGTCGAGGAGTCGCGCCAGGCGCTGGACAAGTACACCGTCGACATGACCAAGCGCGCCGAGGAAGG
CAAGCTCGACCCGGTGATCGGTGCGGACGACGAGATCCGCCGGACCATCCAGGTCTGACGCGGCGGACCAAGAACAACC
CGGTGCTGATCGGCGAACCCTGGCGTGGCAAGACCGCCATCGTCGAGGGCTGGCCACGCGCATCATCAACGGCGAAGTG
CCGGACGGCCTCAAGGACAAGCGCCTGCTGGCCCTGGACATGGGGGCGCTGATCGCCGGTGCCAAGTTCGCGGCGGAGTT
CGAGGAACGCCTGAAGGCGGTCTCTCAACGAACCTGGGCAAGCAGGAAGGCCGGGTTCATCCTGTTTCATCGACGAACCTGCACA
CCATGGTTCGGCGCCGGCAAGGCGGAAGGTGCCATGGACGCCGGCAACATGCTCAAGCCGGCTCTGGCGCGCGGCGAGCTG
CACTGCGTTCGGTCTACTACCTTCGACGAGTATCGCCAGTACATCGAGAAGGATGCCGCGCTGGAGCGCCGCTTCCAGAA
GGTCTGGTGGACGAACCGAGCGAGGAAGACACCATCGCCATCCTCCGTGGCCTCAAGGAACGCTATGA

>ORF25110 (SEQ ID NO:294)

CGTTCCTTGAGGCCACGGAGGATGGCGATGGTGTCTTCTCGCTCGGTTTCGTCCACCAGCACCTTCTGGAAGCGGCGCTC
CAGCGCGGCATCCTTCTCGATGTACTGGCGATACTCGTCGAGGGTAGTAGCACCGACGCAGTGCAGCTCGCCGCGCGCCA
GAGCCGGCTTGAGCATGTTGCCGGCGTCCATGGCACCTTCGCTTGGCGGCGCGGACCATGGTGTGCAATTCTGTCGATG
AACAGGATGACCCGGCCTTCTGCTTGGCCAGTTCGTTGAGGACCGCCTTCAGGCGTTCCTCGAACTCGCCGCGGAACTT
GGCACCGGCGATCAGCGCCCCATGTCCAGGGCCAGCAGGCGCTTGTCTTGGGCGCTCCGGCACTTCGCCGTTGATGA
TGGCTGGGCCAGGCCCTCGACGATGGCGGTCTTGGCGACGCCGGGTTCGCCGATCAGCACCGGGTGTCTTGGTCCGC
CGTGCAGGACCTGGATGGTCCGGCGGATCTCGTCGTCGCGACCGATCACCGGGTCGAGCTTGCCTTCTCGGCGCGCTT
GGTCATGTGACGGGTGACTTGTCCAGCGCCTGGCGCGACTCCTCGACGTTTCGGGTGCTTACCGCTTCGCCGCCACGCA
GGTTGGCCACGGCATTCTCCAGCGCCTTGGCGGACACGCCCTGGCCGAGCAGCAGCTTGGCGAGCCTGGTGTCTCGTCC
ATCGCGGCCAGCAATACCAGCTCGCTGGAGATGAACTGGTCGCCCTTCTGCTGGGCCAGGCGGTGAGCTGGTTGAGCAG
GCGTGCAGATCCTGGGACAGGTTACGTCGCCGTCGGGCTCTGGATCTTCCGCGAGCGGTCGAGTTCTTTGTTGAGGC
CGCTGCGCAGGCGGCGGATATCGAAGCCGACCTGCATCAGCAGGGGCTTGATCGAACCCTTGTGCTCGAGCAGGGCG
GAAAGCAGGTGCACCGGCTCGATGGCCGGATGGTCATGGCCAACGGCCAGGACTGGGCGTCGGAGAGCGCCAGTTGCAG
CTTGCTGGTCAAACGGTCTATTTCGATGGTTCGTCCTTCTATAGAGCGGGCCGGAACGATGGGTGTCCCTGA

>ORF25510 (SEQ ID NO:296)

TGCGCTGGGCCAGGCCCTCGACGATGGCGGTCTTGCCGACGCCGGGTTCGCCGATCAGCACCGGGTGTCTTGGTCCGC
CGCTGCAGGACCTGGATGGTCCGGCGGATCTCGTCGTCGCGACCGATCACCGGGTCGAGCTTGCCTTCTCGGCGCGCTT
GGTCATGTGACGGTGTACTTGTCCAGCGCCTGGCGCGACTCCTCGACGTTTCGGGTGCTTACCGCTTCGCCGCCACGCA
GGTTGGCCACGGCATTCTCCAGCGCCTTGGCGGACACGCCCTGGCCGAGCAGCAGCTTGGCGAGCCTGGTGTCTCGTCC
ATCGCGGCCAGCAATACCAGCTCGCTGGAGATGA

>ORF26762c (SEQ ID NO:298)

CCGCCGACTGCCTGCCGGCGTTGTTCTGCGACCGCTCGGGCACCCGGGTGGCCGGGCCCCATGCCGGCTGGCGCGGGCTG
GCGGCGGGCGTGTGGAGGCGACGGTGGACAGCCTGGGCGTGCCCGGCGACGAAGTGTGGTCTGGCTGGGGCCGGCGAT
CGGCCCCGAGGCCTTCGAGGTGCGCGCGGAGGTCCGCGATGCATTCGTGCTGCGCACGCCGAGGCGCGCTCGGCTTTTCG
TACCTAGCGCCAATCCGGGCGGCTTCATGGCCGACATCTACCGACTCGCGCGGATCCGCCCTGGGCGGCCATGGCGTCACC
GCCGTGCATGGCGGCGGCTTCTGCACCTTCAGCGATACCGCGCGCTTCTATTCTACCGCGCTCGTCGCGTACCGGCCG
TTTTGCCAGCCTGGTCTGGCTCCAGGACTAGGCCCGCGCAGGTTATCCGGCGGCAACTGACCGATGTACAGGTCCGGTCCG
CTTGAACCGCGGAAAATCGCCCTTATCTACTGA

>ORF26257 (SEQ ID NO:300)

ATAAGGGCGATTTCGCGGTTCAAGCGACCGGACCGTGACATCGGTGAGTTCGCCCGGATAACCTGCGCGGGCCTAGT
CCTGGAGCCAGACCAGGCTGGCAAAACGGCCGGTACGCGACGAGCGCGGTAGGAATAGAAGCGCGGGTATCGCTGAAG
GTGCAGAAAGCCGCCCATGCACGGCGGTGACGCCATGGGCGCCAGGCGGATCCGCGGAGTCGGTAGATGTGGCCAT
GAAGCGGCGCGGATTGGCGCTAGGTACGAAAGCCGAGCGCGCTCGGCGTGCGCAGCGACGAATGCATCGCGGACCTCGC
CGCCGACCTCGAAGGCTGCGGGCGATCGCCGGCCCCAGCCAGACAGCAGTTCGTGCGCGGGCACGCCAGGCTGTCC
ACCGTCGCTCCAGCACGCCCGCCGCGAGCCCGCGCCAGCCGGCATGGGCGCGGGCACCCGGGTGCCCGAGCGGTGCGA
GAACAACCGCGGAGGAGTCGGCGGTGATGATCGTACAGGCGACGCCCGGCATCGCGCTCCAGCTGGCGTGGCCCTGA
GCACCGGTTGCGGTGCGGCTCCACCAGTCACTCCGTGCACCTATTCCAACAGCTCGGCCCGCATTCAGACGCTCGGT
CAGGCGTCGGCGGTTTTATTCCACGGCGCGCGGATCGTCTAGACGTGGGCGCAAGGTTGAGACTGTGCAAGGGTGCCT
GGCTGA

>ORF26844c (SEQ ID NO:302)

CGTGGTGGAGGCGACCCGAACCGGTGCTCAGGGCCGACGCCAGCTGGAGCGCGATGCCGGGCGTCGCCTGTACGATCAT
GACCGCCGACTGCCTGCCGGCGTTGTTCTGCGACCGCTCGGGCACCCGGGTGGCCGGGCCCCATGCCGGCTGGCGCGGGC
TGGCGGCGGGCGTGTGGAGGCGACGGTGGACAGCCTGGGCGTGCCCGGCGACGAAGTGTGGTCTGGCTGGGGCCGGCG
ATCGGCCCGCAGGCCTTCGAGGTGCGCGCGGAGGTCCGCGATGCATTCGTGCTGCGCACGCCGAGGCGCGCTCGGCTTT
CGTACCTAGCGCCAATCCGGGCGGCTTCATGGCCGACATCTACCGACTCGCGCGGATCCGCCCTGGGCGGCCATGGCGTCA
CCGCCGTGCATGGCGGCGGCTTCTGCACCTTCAGCGATACCGCGCGCTTCTATTCTACCGCGCTCGTCGCGTACCGGC
CGTTTTGCCAGCCTGGTCTGGCTCCAGGACTAG

>ORF26486 (SEQ ID NO:304)

ATGTCGGCCATGAAGCGGCGCGGATTGGCGCTAGGTACGAAAGCCGAGCGCGCTCGGCGTGCGCAGCGACGAATGCATC
GCGGACCTCGCCGCCGACCTCGAAGGCTGCGGGCGGATCGCCGGCCCCAGCCAGACAGCAGTTCGTGCGCGGGCACGC
CCAGGCTGTCCACCGTCGCCTCCAGCACGCCCGCGCGCAGCCCGCGCCAGCCGGCATGGGCGCGGGCACCCGGGTGCC
GAGCGGTGCGAGAACACGCCGCGGAGGAGTCGGCGGTGATGATCGTACAGGCGACGCCCGGCATCGCGCTCCAGCTGGC
GTGCGCCCTGAGCACCGGTTGCGGTGCGGCTCCACCAGTCACTCCGTGCACCTATTCCAACAGCTCGGCCGGCATTC
AGACGCTCGGTGAGCGTGGCGGTTTTATTCCACGGCGCGCGGATCGTCTAGACGTGGGCGCAAGGTTGAGACTGTC
GAAGGGTGCTGGTGAACCGGCACTGCGCGTGGTCACGAGGCGCGCACACGGGCGGCGCGGCGGCGGCGGCGGCGG
GCCAGGCGTTCAACCGACGAACGCCCTCGCGATCCTGGCGCAACAGGCTGAGCAGCCAGAGGAATTCTTCCGGCAGCGGCG
ATTCACACTTCATGCGCACGCCGGTGGCCGGGTGA

>ORF26857c (SEQ ID NO:306)

GTGCACGGAGTGACGTGGTGGAGGCGACCCGAACCGGTGCTCAGGGCCGACGCCAGCTGGAGCGCGATGCCGGGCGTCCG
CCTGTACGATCATGACCGCCGACTGCCTGCCGGCGTTGTTCTGCGACCGCTCGGGCACCCGGGTGGCCGGGCCCCATGCC
GGCTGGCGCGGGCTGGCGGCGGGCGTGTGGAGGCGACGGTGGACAGCCTGGGCGTGCCCGGCGACGAAGTGTGGTCTG
GCTGGGCGCGGCGATCGGCGCGCAGGCTTCGAGGTGCGCGGCGAGGTCCGCGATGCATTCGTGCTGCGCACGCCGAGG
CGCGCTCGGCTTTCGTACCTAG

>ORF27314c (SEQ ID NO:308)

AGTGGGAATCGCCGCTGCCGAAGAATTCTCTGGCTGCTCAGCCTGTTGCGCCAGGATCGCGAGGCGTTCTGCGGTTGA
ACGCCTGGCTGACCCCGACTGGCCGGCGCCGGCCGTGTGCGGGCCTGCGTGACCAACGCGCAGTGGCGGGGTGAGCCAG
GCACCTTCGACAGTCTGAACCTTGGCGCCACGTCTACGACGATCCGCGCGCGTGGAATAAAACCGCCGACGCCTGAC
CGAGCGTCTGGAATGCCGGCGGAGCTGGTTGGAATAGGTGCACGAGTGACGTGGTGGAGGCCGACCCGAACCGGTGCTC
AGGCGCGACCCAGCTGGAGCGCGATGCCGGCGTCCGCTGTACGATCATGA

Fig. 3-24

>ORF27730c (SEQ ID NO:310)

CAAGCCCGCCGGCCTGGTGGTCCATCCGGCTGCCGGCCATCAGGACGGCACCCCTGCTGAATGCCTTGCTCTACCATGTCC
CGGACATCGCCAATGTGCCGCGCGCCGGGATCGTCCACCGCCTGGACAAGGACACGACCGGCCTGATGGTAGTGGCCAAG
ACGCTGGAGGCCACACCAAGCTGGTGGCGCAACTGCAGGCACGGTCGGTCAGCCGCATCTACGAGGCGATCGTGATCGG
CGTGATCACCTCCGGCGGCACCATCGATGCGCCGATCGGACGGCATGGCGTGACGCGGCAGAAGATGGCGGTGGTCGACG
CCGGCAAGGTGGCGGTGAGCCATTACCGCGTGCTGGAACGCTTCCGTGCGCACACCCATACCCGGGTCAAGCTGGAGACC
GGGCGTACCCACAGATCCGCGTGACATGAGCCATATTGGCTATCCCCTGGTCGGCGATCCGCTCTACGGTGGGCGCTT
CAGGATTCCCCCGGTGGCCAGCCAGACCCTGGTCCAGACTCTTCGCGAATTCCCCCGGCAGGCGCTGCACGCGCGCTTCC
TCGAACTGGATCACCCGGCCACCGCGCTGCGCATGAAGTGGGAATCGCCGCTGCCGGAAGAAATTCCTCTGGGTGCTCAGC
CTGTTCGCGCAGGATCGCGAGGCGTTCTGTGGTTGAACGCTGGCTGACCCCGACTGGCCGGCGCCGGCCCGTGTGCGG
GCCTGCGTGACACGCGCAGTGGCGGGGTGAGCCAGGCACCCCTTCGACAGTCTGAACCTTGGCGCCACGCTCTACGACGA
TCCGCGCGCGTGAATAA

>ORF26983 (SEQ ID NO:312)

CCCCGCCACTGCGGTGGTCACGCAGGCCCGCACACGGGCGGGCGCCGGCCAGTCGGGGGTGAGCCAGGCGTTCAACCGA
CGAACGCTCGCGATCCTGGCGCAACAGGCTGAGCAGCCAGAGGAATTCTTCCGGCAGCGGCGATTCCCACTTCATGCGC
ACGCCGGTGGCCGGGTGATCCAGTTTCAGGAAGCGCGCTGCAGCGCTGCCGGGGGAATTCGCGAAGAGTCTGGACCAG
GGTCTGGTGGCCACCGGGGAATCCTGAAGCGCCACCGTAGACCGGATCGCCGACCAGGGGATAGCCAATATGGCTCA
TGTGACGCGGATCTGGTGGGTACGCGCGGTCTCCAGCTTGACCCGGGTATGGGTGTGCGCACGGAAGCGTTCCAGCACG
CGGTAATGGGTGACCGCCACCTTGCCGGCGTCGACCACCGCCATCTTCTGCCGCTGCACGCCATGCCGTCCGATCGGCGC
ATCGATGGTGCCCGCGAGGTGATCAGCCGATCAGATCGCCTCGTAGATGCGGCTGACCGACCGTGCCTGCAGTTGCG
CCACCAGCTTGGTGTGGGCTCCAGCGTCTTGGCCACTACCATCAGGCCGGTCGTGTCTTGTCCAGGCGGTGGACGATC
CCGGCGCGGGCACATTGGCGATGTCCGGGACATGGTAGAGCAAGGCATTGACGAGGCTGCCGTCTGATGGCCGGCAGC
CGGATGGACCACAGGCCGGCGGGCTTGTCAATCACCAGGATGTGCTCGTCTCGTAGACGATTCCAGCTCGATGTCTT
GTGCGAGCCACTCGCCTGGGCTTCTGCTCGGCTCCAGGACAGTTGCGCGCGCTGTGGACGATGTGCGCGGGCGC
AGCACGGCGCGCTCGACGGTCAGGCGACCGTCTTGTATCCAGCCGGCCAGACGGGAGCGGGAGTGTTCGGGAAAAGCTG
GGCGGCGATCTGGTCGAGACGCTGGCCACCCAGCTCGAACGGCACCTCGGCCGCGCTTGAATCATATCGGACATGAGTA
G

>ORF28068c (SEQ ID NO:314)

CCACAGCGCTAGCCGATTCCAAAAGCCGCGTGAAGCATCGTCTCTACTCATGTCCGATATGATTCAACGCGCGGCCGA
GGTGCCGTTTCGAGCTGGGTGGCCAGCGTCTCGACCAGATCGCCGCCAGCTTTTCCCGAACCTCCCGCTCCCGTCTGG
CCGGTGGATCAAGGACGGTCGCTGACCGTCGACGGCGCGGTGCTGCGCCCGCGCGACATCGTCCACAGCGCGCGCAA
CTGGTCTGGAGGCCGAGCAGGAAGCCAGGGCGAGTGGCTCGCACAGGACATCGAGCTGGAATCGTCTACGAGGACGA
GCACATCCTGGTGATTGACAAGCCCGCCGGCTGGTGGTCCATCCGGCTGCCGGCCATCAGGACGGCACCCCTGCTGAATG
CCTTGCTCTACCATGTCCCGGACATCGCCAATGTGCCGCGCGCGGGATCGTCCACCGCCTGGACAAGGACACGACCGGC
CTGATGGTAGTGGCCAAGACGCTGGAGGCCACACCAAGCTGGTGGCGCAACTGCAGGCACGGTCGGTCAGCCGCATCTA
CGAGGCGATCGTGATCGGCGTGATCACCTCCGGCGGCACCATCGATGCGCCGATCGGACGGCATGGCGTGACGCGCAGA
AGATGGCGGTGGTCGACGCGCGCAAGGTGGCGGTGAGCCATTACCGCGTGCTGGAAACGCTTCCGTGCGCACACCCATACC
CGGGTCAAGCTGGAGACCGGGCGTACCCACAGATCCGCGTGACATGAGCCATATTGGCTATCCCCTGGTCGGCGATCC
GGTCTACGGTGGGCGCTTCAGGATTCCCCCGGTGGCCAGCCAGACCCTGGTCCAGACTCTTCGCGAATTCCCCCGGCAGG
CGCTGCACGCGCGCTTCTCGAACTGGATCACCCGGCCACCGCGGTGCGCATGAAGTGGGAATCGCCGCTGCCGGAAGAA
TTCCTCTGGCTGCTCAGCCTGTTGCCAGGATCGCGAGGCGTTCGTGGTTGA

>ORF27522 (SEQ ID NO:316)

CCGACCGTGCTGAGTTGCGCCACCAGCTTGGTGTGGGCTCCAGCGTCTTGGCCACTACCATCAGGCCGGTCTGTGTC
TTGTCCAGGCGGTGGACGATCCCGCGCGCGGCACATTGGCGATGTCCGGACATGGTAGAGCAAGGCATTACGAGGGT
GCCGTCTGATGGCCGCGAGCCGGATGGACCACAGCCGGCGGGCTTGTCAATCACCAGGATGTGCTCGTCTCGTAGA
CGATTTCCAGCTCGATGTCTGTGCGAGCCACTCGCCTGGGCTTCTGCTGCGCCTCCAGGACAGTTGCGCGCGCGT
TGGACGATGTGCGCGGGCGCAGCACGGCGCGCTCGACGGTCAGGCGACCGTCTTGA

Fig. 3-25

>ORF28033c (SEQ ID NO:318)

GCATCGTCTCCTACTCATGTCCGATATGATTCAACGCGCGGCCGAGGTGCCGTTTCGAGCTGGGTGGCCAGCGTCTCGACC
AGATCGCCGCCCAGCTTTTTCCCGAACACTCCCGCTCCCGTCTGGCCGGCTGGATCAAGGACGGTCGCCTGACCGTCGAC
GGCGCCGTGCTGCGCCCGCGCGACATCGTCCACAGCGCGCGCAACTGGTCCTGGAGGCCGAGCAGGAAGCCAGGGCGA
GTGGCTCGCACAGGACATCGAGCTGGAAATCGTCTACGAGGACGAGCACATCCTGGTGATTGA

>ORF29701c (SEQ ID NO:320)

TCTTCCAGTTCGCTGGAGATCAGCAGGACCAGTACCAGGCCGATGGTCAGGCGGTACAGGTGGTACAGACGGAGGATGCG
TTGCCCTGCTCCTCGCTCAGCCGTAGCCGTTTACGCGCGCAGGTCGCCCTGGTCTGGCCGAGGTGCGCCTGGCTGCAA
TACCAGCGTTGTTCTGGGCGAGGGCGTTGGCCTGCGGCACGTGGACGCCGCAATGGGCGCAGCGGACCATCGGCGATGC
GCTCGGCTCGTCTGCGGACGTTGCTGCTGGCGCGGAGTGGGACGGGTAAAGCGACGCCAGCCAGAACCGCATGGCGA
TCAGGGCGATCCAGAACAGGAGGCGGAAAAGGCCCATGGTGATCTCGGAGGCTGGAGAAAGCTGCAGTTTAGCCAAGCCG
CCGGCTCGATCCCAGACGGGAAGGTCCAGGCTGTGCGGCGTTTGGCGCTGGGAGAGGCATGGCGCGGGCAAAAAGAAGG
GAGGCTGCGCCTCCCTTCGGTGTTCGTGCGATCAGTCGAAGAGACCGAAGGTTCATGTCCACCAGGAGCGACCGG
AGTCTCTGTCGTATCGTCTCCTCGGCTTCTCGTCTGCGGCGCTGTGATCCTGGTTCCTGGCTTCAGTTTCGGCGGGGATC
TCCCGCTCGGCATCCTCGTACTGCTTGATCAGTCCCTTGGCGGCTGGGTTCATGTGCGGCGGCGGCTCGCCGCTTC
GATCAGGCCCAGGGTGGCCTTGGCCAGCCAGGAGCGGGTGTGCGCCTCGCTTCGCGGGCGACGAACTCGCCATCCTTGA
GGCTGGCGTTATCCGGATAGTTTACGCTTGAAGGTTTCCAGGCTGGTGTGCTGGCCAGGTCGTGAGACCCAGGCGACGGTAG
GCTTCGACCATGATCGCCAGGCCATCGCCGACGGCCGGGTTTCTGGAAGTTCTCCACCAGTAGCGACCGCGGTTGGC
GGCGGCGACATAGGCCCTGGCGCTTTCAGGTAGTAGTGGCGGACGTGCATTCGTAGGCCCGCCAGCAGGTTGCGCAGGTACA
CCATGCGCGCCTTGGCGTCCGGGCGTAGCGGCTGTGGGGAAGCGGCTGGTGAGCTGGGCGAACTCGTTGAAGGAGTCCG
CGGGCGGCGCCCGGCTCGGCTTGGTTCATGTCCAGCGGCAAGAGCGCGCCAGCAGGCGCGGCTCCTGGTGAAGGAGGA
CAGGCTTTGAGGTAGTAGGCTAGTCGACGTTGGGCTGTGCGGATGCAGGCGGATGAAGCGTTTCGGCGGCGGCGCGG
CGGCTTCGGGCTCCATGTTCTTGTAGTTGGCGTAGATCAGCTCGAGCTGGGCTGCTCGGCGTAGCGGCCGAAGGGATAG
CGCATTCGAGGGCTTTTACGCTTGGTGACGGCGCTGTTGTAGCTCTTGTGTTGAGGTGCTCCTGCGCCTGCTGGTACAG
CTGGCTCTCGCTCAGGTTCTCGTCGACAGTCTCCTTGTTCGAGGAGCAGGCTGCGGTGAGGGCGAGGATGGCGATCAGCA
GCAGGTGTTTCACTTGCATGGCGGCTTGCCTCCCTGGGACGGTCGGCTTGGCTCAACCGTCTGTTATGA

>ORF28118 (SEQ ID NO:322)

CAGACGGTTGAGGCCAAGCCGACCGTCCCAGGGACGCAAGCCGCCATGCAAGTGAAACACCTGCTGCTGATCGCCATCCT
CGCCCTCACCGCAGCCTGCTCCTCGAACAAGGAGACTGTGACGAGAACTGAGCGAGAGCCAGCTGTACCAGCAGGCGC
AGGACGACCTCAACAACAAGAGCTACAACAGCGCCGTACCAAGCTGAAAGCCCTCGAATCGCGCTATCCCTTCGGCCGC
TACGCCGAGCAGGCCCAGCTCGAGCTGATCTACGCCAACTACAAGAACATGGAGCCCCGAAGCCGCCCGCGCCGCCGCA
ACGCTTCATCCGCTGCATCCGCGACCCCCAACGTGACTACGCTACTACCTCAAAGGCCTGTCTCCTTCGACCAGG
ACCGCGGCTGCTGGCGGCTTCTGCGGCTGGACATGACCAAGCGCGACCCGGGCGCCGCCGCGACTCCTTCAACGAG
TTCGCCCAGCTCACCAGCGCTTCCCCAACAGCCGCTACGCCCCGACGCCAAGCGCGCATGGTGACCTGCGCAACCT
GCTGGCGGCTACGAAGTGACGTCGGCCACTACTACCTGAAGCGCCAGGCTATGTGCGCGCCGCCAACCGCGGTGCT
ACGTGGTGGAGAACTTCCAGGAAACCCGGCCGTGGCGATGGCCTGGCGATCATGGTGAAGCCTACCGTCGCTGGGT
CTCGACGACCTGGCCAGCACCAGCCTGGAACCCCTCAAGCTGAACTATCCGGATAACGCCAGCCTCAAGGATGGCGAGTT
CGTCGCCCGGAAAGCGAGGCCGACACCCGCTCCTGGCTGGCCAAGGCCACCTGGGCGCTGATCGAAGCGGCGAGCCGC
CGCCGCACATGGAAACCCAGGCCGCCAAGGACGTGATCAAGCAGTACGAGGATGCCGAGCGGGAGATCCCCGCCGAAGTG
AAGCCGGAACCCAGGATCACAGCGCCGACGACGAGAAGCCGGAGAGCGATGACGACGAGGACTCCGGTCGCTCCTGGTG
GAGTACATGACCTTCGGTCTCTTCGACTGA

>ORF28129 (SEQ ID NO:324)

GGCCAAGCCGACCGTCCCAGGGACGCAAGCCGCCATGCAAGTGAAACACCTGCTGCTGATCGCCATCCTCGCCCTCACCG
CAGCCTGCTCCTCGAACAAGGAGACTGTGACGAGAACTGAGCGAGAGCCAGCTGTACCAGCAGGCGCAGGACGACCTC
AACAACAAGAGCTACAACAGCGCCGTACCAAGCTGAAAGCCCTCGAATCGCGCTATCCCTTCGGCCGCTACGCCGAGCA
GGCCAGCTCGAGCTGATCTACGCCAACTACAAGAACATGGAGCCCCGAAGCCGCCCGCGCCGCCGCGAACGCTTCATCC
GCCTGCATCCGCGACACCCCAACGTGACTACGCTACTACCTCAAAGGCCTGTCTCCTTCGACCAGGACCGCGGCTG
CTGGCGGCTTCTGCGGCTGGACATGACCAAGCGCGACCCGGGCGCCGCCGCGACTCCTTCAACGAGTTTCGCCAGCT
CACCAGCCGCTTCCCCAACAGCCGCTACGCCCCGACGCCAAGCGCGCATGGTGACCTGCGCAACCTGCTGGCGGCT
ACGAAGTGACGTCGGCCACTACTACCTGAAGCGCCAGGCTATGTGCGCGCCGCCAACCGCGGTGCTACGTGGTGGAG
AACTTCCAGGAAACCCGGCCGTGGCGATGGCCTGGCGATCATGGTGAAGCCTACCGTCGCTGGGTCTCGACGACCT
GGCCAGCACCAGCCTGGAACCCCTCAAGCTGAAGTATCCGGATA

Fig. 3-26

>ORF29709c (SEQ ID NO:326)

GGACCTGATCTTCCAGTTTCGCTGGAGATCAGCAGGACCAGTACCAGGCCGATGGTCAGGCGGTACAGGTGGTACAGACGG
AGGATGCGTTGCCCTGCTCCTCGCTCAGCCGTAGCCGTTAGCGCGCACGGTCGCCCTGGTCTGGCGCAGGTGCGCCT
GGCTGCAATACCAGCGTTGTTCTGTTGGGCGAGGGCGTTGGCCTGCGGCACGTGGACGCCGAATGGGCGCAGCGGACCATC
GGCGATGCGCTCGGCTCGTCTGCGGACGTTGCTGCTGGCGCGGAGTGGGACGGGTAAAGCGACGCCAGAGCCAGAACGC
GATGGCGATCAGGGCGATCCAGAACAGGAGGGCGGAAAAGGCCCATGGTGATCTCGGAGGCTGGAGAAAGCTGCAGTTTAG
CCAAGCCGCCGGCTCGATCCCAGACGGGAAGGTCCAGGCTGTGCGGCGTTTGGCGCTGGGAGAGGCATGGCGGCGGGCAA
AAAGAAGGGAGGCTGCGCCTCCCTTCGGTGTTTCGTGCGATCAGTCGAAGAGACCGAAGGTCATGTAG

>ORF29189 (SEQ ID NO:328)

TCGCACGAAACACCGAAGGGAGGCGCAGGCCTCCCTTCTTTTGGCCGCCGCCATGCCTCTCCAGCGCCAAACGCCGCA
CAGCCTGGACCTTCCCGTCTGGGATCGAGCCGGCGGCTTGGCTAAACTGCAGCTTTCTCCAGCCTCCGAGATCACCATGG
GCCTTTTCGCCCTCCTGTTCTGGATCGCCCTGATCGCCATCGCGTTCTGGCTCTGGCGTCGCTTTACCCGTCCCACTCCG
CGCCAGCAGCAACGTCCGCAGGACGAGCCGAGCGCATCGCCGATGGTCCGCTGCGCCATTGCGGCGTCCACGTGCCGCA
GGCCAAAGCCCTCGCCACGAACAACGCTGGTATTGCAGCCAGGCGCACCTGCGCCAGGACAGGGCGACCGTGCAGCGCT
GA

>ORF29382 (SEQ ID NO:330)

TCGCCATCGCGTTCTGGCTCTGGCGTCGCTTTACCCGTCCCACTCCGCGCCAGCAGCAACGTCCGCAGGACGAGCCGAGC
GCATCGCCGATGGTCCGCTGCGCCCATTCGGCGCTCCACGTGCGCGCAGGCCAACGCCCTCGCCACGAACAACGCTGGTA
TTGCAGCCAGGCGCACCTGCGCCAGGACAGGGCGACCGTGCAGCGCTGAACGGCTACGGCTGAGCGAGGAGCAGGGGCAA
CGCATCCTCCGTCTGTACCACCTGTACCGCCTGACCATCGGCCTGGTACTGGTCTCTGATCTCCAGCGAACTGGAAGA
TCAGGTCTCAAGCTCGTCCACCCTGAACTGTTCCATGTGCGGAGTTGGTGCTACCTGGTCTTCAACATCCTGGTCGCGC
TGTTCTGCGCGCGTTCGCGGCAATTGCTGCGGATCTTCATCCTCGCGCTCACCGACGTGCTGATGCTTTGCGGCGCTGTT
TACGCAGGTGGCGGCGTACCCAGCGGCATCGGCAGCCTGCTGGTGGTGGCGGTGGCCATTGCCAACATCCTGCTGCGCGG
GCGCATCGGCCTGGTCATCGCGGCGGCGGCCAGCCTCGGCCTGCTCTACCTGACCTTCTTCTCAGCCTGAGCAGTCCGG
ACGCCACCAACCACTACGTCCAGGCCGGCGGCTCGGCACCCTGTGCTTCGCCGCCGCGCTGGTGATCCAGGCTCTGGTG
CGGCGCCAGGAGCAGACCGAAACGCTGGCCGAAGAACGCGCCGAGACGGTCGCCAACCTGGAGGAACTCAACGCATTGAT
CCTGCAGCGCATGCGCACCGGCATCCTCGTGGTCGATAGCCGTGAGGCCATCCTCCTCGCCAACAGGCCGCCCTCGGCC
TGCTCAGGCAGGACGACGTGCAGGGCGCCAGCCTCGGCCGCCACAGCCCGATGCTGATGCACTGCATGAAGCAATGGCGC
CTGAATCCCAGCCTCCGTCCGCCGACGCTCAAGGTGGTGCCGATGGCCGACGGTGCAACCCAGCTTTATCAGCCTCAA
CCGCGAAGACGACGACGACGTGCTGATCTTCTCGAAGACATTTGCGAGATCGCCAGCAGCGCAGCAGATGAAGCTGG
CCGTCCTTGGCGCCTGACCGCGGCATCGCCCATGAGATCCGCAACCGCTGGGCGCGATCAGCCACGCCGCCCACTG
CTGCAGGAGTCAGAGGAACTGGATGCCCCGACCGACGCTGACGCGATCATCCAGGACAGTCGAAGCGGATGAACCT
GGTCATCGAGAACGTCCTGCAGCTCTCCCGTCGCCGCCAGGCCGAACCGCAGCAGCTCGACCTGAAGGAGTGGCTTCAGC
GGTTCGTGAGCAATAACCCGGCAGGCTGCGCAACGACAGCCAACTGCACCTGCAGCTCGGTGCGGCGGACATCCAGACC
CGCATGGACCCACACAGTTGAACAGGTGCTGAGCAACCTGGTGCAGAACGGTCTTCGCTACAGCGCCAGGCGCACGG
GCGCGGCCAGGTCTGGCTGAGCCTCGCGCGCGACCCGAGAGCGACCTGCCGGTGTGGAAGTCATCGACGACGGTCCCG
GCGTACCGGCGGACAACTGAACAACCTGTTCAACCCCTCTTTACTACAGAAAGCAAAGGCACCGGCTGGGCTCTAT
CTCTCCCGCAACTCTGCGAGAGCAACAGGCACGGATCGACTACCGCAATCGCGAGGAAGGCGGCGCTGCTTCCGCAT
CACCTTCGCCACCCGCGCAAACTCAGCTGA

Fig. 3-27

>ORF30590c (SEQ ID NO:332)

CTCTGCAGCAGTTGGGCGGCGTGGCTGATCGCGCCAGCGGGTTGCGGATCTCATGGGCGATGCCGGCGGTGAGGCGGC
CAAGACCGGCCAGCTTCATCTGCTGCGCCTGCTGGGCGATCTGCGAAATGTCTTCGAGGAAGATCAGCACGTGCTGGTCCG
TCTTCGCGGTTGAGGCTGATAAAGCTGGGTTGCACCGTCGGGCCATCCGGCACCACCTTGAGCGTCGGCGGACGGAGGCT
GGGATTCAGGCGCCATTGCTTCATGCAGTGCATCAGCATCGGGCTGTGGCGGCCGAGGCTGGCGCCCTGCACGTCGTCTCT
GCCTGAGCAGGCCGAGGGCGGCCTGGTTGGCGAGGAGGATGGCCTGACGGCTATCGACCACGAGGATGCCGGTGCGCATG
CGCTGCAGGATCAATGCGTTGAGTTCCTCCAGGTTGGCGACCGTCTCGGCGCGTTCCTTCGGCCAGCGTTTCGGTCTGCTC
CTGGCGCCGCACCAGAGCCTGGATCACCAGCGCGCGCGGAAGCACAGGGTGCCGAGGCGCGCGCCTGGACGTAGTGGT
TGGTGGCGTCCGACTGCTCAGGCTGAGGAAGAAGGTGAGGTAGAGCAGGCCGAGGCTGGCGCGCGCGCGATGACCAGG
CCGATGCGCCCGCGCAGCAGGATGTTGGCAATGGCCACCGCCACCAGCAGGCTGCCGATGCCGTGGGTACGCCGCC
ACCTGCGTAGAACAGGCCGCAAAGCATCAGCACGTGCGTGAGCGCGAGGATGAAGATCGGCAGCAATTGCCCGACGGCG
GCAGGAACAGCGCGACCAGGATGTTGAAGACCAGGTAGCACCAACTGCCGACATGGAACAGTTGAGGGTGGACGAGCTTG
AGGACCTGATCTTCCAGTTCGCTGGAGATCAGCAGGACCAGTACCAGGCCGATGGTCAGGCGGTACAGGTGGTACAGACG
GAGGATGCGTTGCCCTGCTCCTCGCTCAGCCGTAG

>ORF29729 (SEQ ID NO:334)

ACTGTTCCATGTCGGCAGTTGGTGCTACCTGGTCTTCAACATCCTGGTCGCGCTGTTCTTCCGCGCGTTCGGGCAATTGC
TGCCGATCTTCATCTCGCGCTCACCGACGTGCTGATGCTTTGCGGCCCTGTTCTACGCAGGTGGCGCGGTACCCAGCGGC
ATCGGCAGCCTGCTGGTGGTGGCGGTTGGCCATTGCCAATCTCTGCTGCGCGGGCGCATCGGCCTGGTTCATCGCGCGGC
GGCCAGCCTCGCGCTGCTCTACCTGACCTTCTTCTCAGCCTGAGCAGTCCGGACGCCACCAACCACTAGTCCAGGCCG
GCGCCCTCGGCACCTTGTGTTTCGCGCGCGCGCTGGTGATCCAGGCTCTGGTGCGGCGCAGGAGCAGACCGAAACGCTG
GCCGAAGAACGCGCCGAGACGGTCGCCAACCTGGAGGAACTCAACGCATTGATCCTGCAGCGCATGCGCACCGGCATCTT
CGTGGTCGATAG

>ORF30221 (SEQ ID NO:336)

CCGTGAGGCCATCCTCCTCGCCAACCAGGCCGCCCTCGGCCGTGCTCAGGCAGGACGACGTGCAGGGCGCCAGCCTCGGCC
GCCACAGCCCGATGCTGATGCACTGCATGAAGCAATGGCGCTGAATCCCAGCCTCCGTCCGCCGACGCTCAAGGTGGTG
CCGGATGGCCCGACGGTGCAACCCAGCTTTATCAGCCTCAACCGGAAGACGACGACGCTGCTGATCTTCTCGAAGA
CATTTTCGAGATCGCCAGCAGGCGCAGCAGATGAAGCTGGCCGGTCTTGCCGCCTGACCGCCGGCATCGCCCATGA

>ORF30736c (SEQ ID NO:338)

AGCCACTCCTTCAGGTGAGCTGCTGCGGTTGCGCCTGGCGGCGACGGGAGAGCTGCAGGACGTTCTCGATGACCAGGTT
CATCCGCTTCGACTGGTCTGGATGATCTGCGTCAGGCGTCGGTCCGGGGCATCCAGTTCTCTGACTCCTGCAGCAGTT
GGGCGCGTGGCTGATCGCGCCAGCGGGTTGCGGATCTCATGGGCGATGCCGGCGGTGAGGCGGCCAAGACCGGCCAGC
TTCATCTGCTGCGCCTGCTGGGCGATCTGCGAAATGTCTTCGAGGAAGATCAGCACGTGCTGGTCTGCTTCGCGGTTGAG
GCTGATAAAGCTGGGTTGCACCGTCGGGCCATCCGGCACCACCTTGAGCGTCGGCGGACGAGGCTGGGATTGAGGCGCC
ATTGCTTCATGCAGTGCATCAGCATCGGGCTGTGGCGGCCGAGGCTGGCGCCCTGCACGTCGTCTGCTGAGCAGGCCG
AGGGCGGCCTGGTTGGCGAGGAGGATGGCCTGA

>ORF30539 (SEQ ID NO:340)

GATCCGCAACCCGCTGGGCGCGATCAGCCACGCCGCCCAACTGCTGCAGGAGTCAGAGGAACTGGATGCCCCGGACCGAC
GCCTGACGCAGATCATCCAGGACAGTCGAAGCGGATGAACCTGGTCATCGAGAACGTCCTGCAGCTCTCCCGTCGCCGC
CAGGCCGAACCGCAGCAGCTCGACCTGAAGGAGTGGCTTCAGCGGTTTCGTCGACGAATAACCCGGCAGGCTGCGCAACGA
CAGCCAACTGCACCTGCAGCTCGGTGCCGGCGACATCCAGACCCGCATGGACCCACACCAGTTGAACAGGTGCTGAGCA
ACCTGGTGAGAACGGTCTTCGCTACAGCGCCAGGGCGCAGGGCGCGGCCAGGTCTGGCTGAGCCTCGCGCGCGACCCG
GAGAGCGACCTGCCGGTGTGGAAGTCATCGACGACGGTCCCGGCGTACCGGCGGACAACTGAACAACCTGTTTGAACC
CTTCTTTACTACAGAAAGCAAAGGCACCGGCCTGGGCCTTATCTCTCCCGGAACTCTGCGAGAGCAACCAGGCACGGA
TCGACTACCGCAATCGCGAGGAAGGGCGCGGCTGCTTCGCGCATCACCTTCGCCACCCCGCGCAAACTCAGTGCAGGAAG
CCGCACGCATGAGCCGACAAAAGCCCTGATCGTCGACGATGAACCGGATATCCGCGAACTGCTGGAATCACTCTCGGC
CGCATGAAGCTGGACACCCGACGCGCCCGCAACGTCAAGGAAGCCGCGAGTTGCTGGCCCGGAGCCGTTGACCTGTGC
CTCACCGACATGCGCCTGCCGACGGCAGCGGCCTCGATCTGGTCCAGTACATCCAGCAGCGCCATCCACAGACCCCGGT
GGCCATGA

>ORF31247c (SEQ ID NO:342)

TTTCCAGCAGTTTCGCGGATATCCGGTTCATCGTCGACGATCAGGGCTTTTTGTGGCTCATGCGTGCGGCTTCCGTGAGC
TGAGTTTGGCGGGTGGGCGAAGGTGATGCGGAAGCAGCCGCCGCTTCTCGCGATTGCGGTAGTCGATCCGTGCCTGG
TTGCTCTCGCAGAGTTCGCGGGAGAGATAGAGGCCAGGCCGGTGCCCTTTGCTTTCTGTAGTAAAGAAGGGTTCGAACAG
GTTGTTCACTTTGTCCGCCGTACGCCGGGACCGTCGTGATGACTTCCAGCACCGGCAGGTGCTCTCCGGGTGCGCGC
CGAGGCTCAGCCAGACCTGGCCGCGCCCGTGGCCTGGGCGCTGTAGCGAAGACCGTTCTGCACCAGGTTGCTCAGCACC
TGGTTCAACTGGTGTGGGTCCATGCGGGTCTGGATGTGCGCGGCACCGAGCTGCAGGTGCAGTTGGCTGTCGTTGCGCAG
CCTGCCGGGGTATTGCTCGACGAACCGCTGAAGCCACTCCTTCAGGTGAGCTGCTGCGGTTGCGCCTGGCGGCGACGGG
AGAGCTGCAGGACGTTCTCGATGACCAGGTTTCATCCGCTTCGACTGGTCTTGATGATCTGCGTCAGGCGTCGGTCCGGG
GCATCCAGTTCCTCTGA

>ORF30963c (SEQ ID NO:344)

CTTCCAGCACCGGCAGGTGCTCTCCGGGTGCGCGCGAGGGCTCAGCCAGACCTGGCCGCGCCCGTGGCCTGGGCGCTG
TAGCGAAGACCGTTCTGCACCAGGTTGCTCAGCACCTGGTTCAACTGGTGTGGGTCCATGCGGGTCTGGATGTCGCCGGC
ACCGAGCTGCAGGTGCAGTTGGTGTGCTTGGCGAGCCTGCCGGGGTATTGCTCGACGAACCGCTGAAGCCACTCCTTCA
GGTCGAGCTGCTGCGGTTGCGCCTGGCGGCGACGGGAGAGCTGCAGGACGTTCTCGATGA

>ORF31539c (SEQ ID NO:346)

GGCGGTTGCCACCAGCTCCCGCAAGCGACCGAGGTGACCGGTTTGGTGAGGAAGTCGAAGGCACCGGCCCTTGAGCGCCT
GGATCGCGGTGTCCAGGCTGCCGTACCGGTGATCATGGCCACCGGGTCTGTGGATGGCGCTGCTGGATGTAAGGACC
AGATCGAGGCCGCTGCCGTCCGGCAGGCGCATGTCGGTGAGGCACAGGTGCAACCGCTCGCGGGCCAGCAACTCGCGGCT
TCCTTGACGTTGCGGGCGCTGCGGGTGTCCAGCTTCATGCGGCCGAGAGTGATTTCCAGCAGTTCGCGGATATCCGGTTC
ATCGTCGACGATCAGGGCTTTTTGTGGCTCATGCGTGCGGCTTCGTCAGCTGA

>ORF31222 (SEQ ID NO:348)

ACCGGATATCCGCGAACTGCTGGAATCACTCTCGGCCGATGAAGCTGGACACCCGAGCGCCCGCAACGTCAAGGAAG
CCGCGAGTTGCTGGCCCGGAGCCGTTTCGACCTGTGCCTCACCGACATGCGCCTGCCGGACGGCAGCGGCCTCGATCTGG
TCCAGTACATCCAGCAGCGCCATCCACAGACCCCGGTGGCCATGATCACCGCGTACGGCAGCCTGGACACCGCGATCCAG
GCGCTCAAGGCCGCTGCCTTCGACTTCCTCACCAAACCGGTGACCTCGGTGCTTGCGGGAGCTGGTGGCAACCGCCCT
ACGCTTGCGCAACCCGGAAGCCGAGGAAGCGCCGGTGGACAACCGCCTGCTCGCGGAGTCGCGCCGATGCGCGCCCTGC
GCAACCAGATCGGCAAGCTGGCGCGCAGCCAGGCGCCGGTCTACATCAGTGGCGAGTCCGGCAGCGGCAAGGAAGTGGTG
GCGCGCTGATCCAGGAGCAGGGGCCACGTATCGAGCGGCCGTTTCGTGCGCGTGAACTGCGCGCGGATTCCTCCGAGCT
GATGGAAGCGAGTTCTTCGGCCACAAGAAAGGCGAGTTCACTGGCGCTATCGAAGACAAGCAGGGCCTGTTCAGGCCG
CCAGCGGTGGCACCTGTTCTTCGACGAAGTCGCCGACCTGCCGATGGCCATGCAGGTCAAAGTCTCGCGGCGATCCAG
GAAAAGGCCGTGCGCGCGGTGCGCGGCCAGCAGGAGGTGCGCGTGCACGTGCGCATCCTCTGCGCCACCCACAAGGACC
TCGCGCCGCAAGTCGCGCGCGGGCGCTTCGCCCAGGACCTCTACTACCGCCTCAACGTATCGAGCTGCGCGTACACCGC
TGCGCGAACGCCGCGAGGACATCCCGCTGCTCGCCGAACGCATCCTCAAGCGCCTGGCCGGCGACACCGGCCTGCCGGC
GCCAGGCTGACCGGCGACGCACAGGAGAAGCTGAAGAACTACCGCTTCCCGGGCAACGTCCGCGAGCTGGAAAAATGCT
GGAGCGCGCTATACCTGTGCGAAGACGACCAGATCCAGCCTCACGACCTGCGCCTGGCCGATGCGCCGGGTGCCAGCC
AGGAAGGCCCGCGAGCCTGAGCGAAATCGACAACCTCGAGGACTACCTGGAAGACATCGAGCGCAAGCTGATCATGCAG
GCACTCGAGGAGACCCGCTGGAACCCGACCGCCGCGGCCAGCGCCTGGGCCTGACGTTCCGCTCGATGCGCTACCGCCT
GAAAAGCTGGGCATCGACTGA

Fig. 3-29

>ORF31266 (SEQ ID NO:350)

AGCTGGACACCCGAGCGCCCGCAACGTCAAGGAAGCCGCGAGTTGCTGGCCCGGAGCCGTTGACCTGTGCCTCACCG
ACATGCGCCTGCCGGACGGCAGCGGCTCGATCTGGTCCAGTACATCCAGCAGCGCCATCCACAGACCCCGGTGGCCATG
ATCACCGCGTACGGCAGCCTGGACACCGCGATCCAGGCGCTCAAGGCCGGTGCCTTCGACTTCCTCACCAAACCGGTCTGA
CCTCGGTTCGCTTGGCGGAGCTGGTGGCAACCGCCCTACGCTTGCGCAACCCGGAAGCCGAGGAAGCGCCGGTGGACAACC
GCCTGCTCGGCGAGTCCGCGCCGATGCGCGCCCTGCGCAACACAGATCGGCAAGCTGGCGCGCAGCCAGGCGCCGGTCTAC
ATCAGTGGCGAGTCCGGCAGCGGCAAGGAACTGGTGGCGCGCCTGATCCACGAGCAGGGGCCACGTATCGAGCGGCCGTT
CGTGGCGGTGAACTGGCGCGGATTCCCTCCGAGCTGATGGAAAGCGAGTTCTTCGGCCACAAGAAAGGCAGCTTCACTG
GCGCTATCGAAGACAAGCAGGGCCTGTTCAGGCCGCCAGCGGTGGCACCCTGTTCTTCGACGAAGTCGCGGACCTGCCG
ATGGCCATCGAGGTCAAACCTGCTCCGGGCGATCCAGGAAAAGGCCGTGCGCGCGGTTCGGCGGCCAGCAGGAGGTGCCGT
CGCACGTGCGCATCCTCTGCGCCACCCACAAGGACCTCGCCGCGGAAGTCGGCGCCGGGCGCTTCGCCAGGACCTCTAC
TACCGCCTCAACGTATCGAGCTGCGCGTACACCGCTGCGCGAAGCCGCGAGGACATCCCGTCTCGCCGAACGCATC
CTCAAGCGCTGGCCGGCAGACCGGCCTGCGGGCCGCGAGGCTGACCGGCGACGCACAGGAGAAGCTGAAGAACTACCG
CTTCCCGGCAACGTCCGCGAGCTGGAAAACATGCTGGAGCGCGCCTATACCCTGTGCGAAGACGACCAGATCCAGCCTC
ACGACCTGCGCCTGGCCGATGCGCCGGGTGCCAGCCAGGAAGGCGCCGCGAGCCTGAGCGAAATCGACAACCTCGAGGAC
TACCTGGAAGACATCGAGCGAAGCTGATCATGCAGGCACTCGAGGAGACCCGCTGGAACCGCACCGCCGCGGCCAGCG
CCTGGGCCTGACGTTCCGCTCGATGCGCTACCGCCTGAAAAGCTGGGCATCGACTGAAAGTGAAAAGGCCTGTCCGAAG
ACAGGCCCTTTGGTTTTCGCTCCTCAGAGGCGACCAGCCGGGGCGTAGGGGGCCGGGTTCGATGA

>ORF31661c (SEQ ID NO:352)

ACCGGCGCCTGGCTGCGCGCCAGCTTGCCGATCTGGTTGCGCAGGGCGCGCATCGGCGGCGACTCGCCGAGCAGGCGGTT
GTCCACCGGCGCTTCTCGGCTTCCGGGTTGCGCAAGCGTAGGGCGGTTGCCACCAGCTCCCGCAAGCGACCGAGGTCTGA
CCGGTTTGGTGAGGAAGTCGAAGGCACCGGCCTTGAGCGCCTGGATCGCGGTGTCCAGGCTGCCGTACGCGGTGATCATG
GCCACCGGGGTCTGTGGATGGCGCTGCTGGATGTAAGTGGACCAGATCGAGGCCGTGCCGTCCGGCAGGCGCATGTCGGT
GAGGCACAGGTCTGAACGGCTCGCGGGCCAGCAACTCGCGGCTTCCTTGA

>ORF32061c (SEQ ID NO:354)

AGGTCTGGCGGAAGCGCCCGCGCGGACTTCGGCGGCGAGGTCTTGTGGGTGGCGCAGAGGATGCGCACGTGCGACGG
CGACCTCTGCTGGCCGCGACCGCGCGCACGGCCTTTTCTGGATCGCCCGGAGCAGTTTGACCTGCATGGCCATCGGC
AGGTTCGGGACTTCGTGAGGAACAGGGTGCCACCGCTGGCGGCTGGAACAGGCCCTGCTTGTCTTCGATAGCGCCAGT
GAAGCTGCCCTTTCTTGTGGCCGAAGAAGTCTGCTTTCCATCAGCTCGGAGGGAATCGCGCCGAGTTACCGGCACGAACG
GCCGCTCGATACGTGGCCCTGCTCGTGGATCAGGCGCGCCACAGTTCTTGGCGCTGCCGACTCGCCACTGATGTAG
ACCGGCGCCTGGCTGCGCGCCAGCTTGCCGATCTGGTTGCGCAGGGCGCGCATCGGCGGCGACTCGCCGAGCAGGCGGTT
GTCCACCGGCGCTTCTCGGCTTCCGGGTTGCGCAAGCGTAG

>ORF32072c (SEQ ID NO:356)

GGCGGTAGTAGAGGTCTTGGCGGAAGCGCCCGCGCGGACTTCGGCGGCGAGGTCTTGTGGGTGGCGCAGAGGATGCGC
ACGTGCGACGGCGACCTCCTGCTGGCCGCGACCGCGCGCACGGCCTTTTCTGGATCGCCCGGAGCAGTTTGACCTGCA
TGGCCATCGGCAGGTTCGGCGACTTCGTGAGGAACAGGGTGCCACCGCTGGCGGCTTGAACAGGCCCTGCTTGTCTTCG
ATAGCGCCAGTGAAGCTGCCTTTCTTGTGGCCGAAGAAGTCTGCTTTCCATCAGCTCGGAGGGAATCGCGCCGAGTTCAC
CGGCACGAACGGCCGCTCGATACGTGGCCCTGCTCGTGGATCAGGCGCGCCACCAGTTCTTGGCGCTGCCGACTCGC
CACTGATGTAG

>ORF31784 (SEQ ID NO:358)

TGGAAGCGAGTTCTTCGGCCACAAGAAAGGCAGCTTCACTGGCGCTATCGAAGACAAGCAGGGCCTGTTCCAGGCCGCC
AGCGGTGGCACCTGTTCTTCGACGAAGTCGCCGACCTGCCGATGGCCATGCAGGTCAAACCTGCTCCGGGCGATCCAGGA
AAAGGCCGTGCGCGCGGTTCGGCGGCCAGCAGGAGGTGCCGCTCGCACGTGCGCATCCTCTGCGCCACCCACAAGGACCTC
GCCGCCGAAGTCGGCGCCGGGCGCTTCCGCCAGGACCTCTACTACCGCCTCAACGTATCGAGCTGCGCGTACACCGCTG
CGGAACGCCGCGAGGACATCCCGTCTCGCCGAACGCATCCTCAAGCGCCTGGCCGGCGACACCGGCCTGCCGGCCGC
CAGGCTGA

Fig. 3-30

>ORF32568c (SEQ ID NO:360)

GGAGCGAAACCAAAGGCCTGTCTTCGGACAGGCCTTTTCACTTTTCAGTCGATGCCAGCTTTTTTCAGGCGGTAGCGCA
TCGAGCGGAACGTCAGGCCAGGCCTGGGCCGCGCGGTGCGGTTCCAGCGGGTCTCCTCGAGTGCCTGCATGATCAGC
TTGCGCTCGATGTCTTCCAGGTAGTCCTCGAGGTTGTGATTTCGCTCAGGCTCGCGGCGCCTTCTGGCTGGCACCCGG
CGCATCGGCCAGGCGCAGGTCGTGAGGCTGGATCTGGTCTGCTTCGCACAGGGTATAGGCGCGCTCCAGCATGTTTTCCA
GCTCGCGGACGTTGCCCGGAAGCGGTAGTTCTTCAGCTTCTCCTGTGCGTCGCGGTCAGCCTGGCGGCGGCGAGGCCG
GTGTGCGCGGCCAGGCGCTTGAAGATGCGTTCGGCGAGCAGCGGGATGTCTCGCGGCGTTCGCGCAGCGGTGTACGCGC
AGCTCGATGACGTTGAGGCGGTAG

>ORF33157c (SEQ ID NO:362)

ACAGACGGAGGTGCGCGGCTGGTTGCGCGACGGCGATCGAGTGGTGGCGTGGCGACCTCGCGTGGCGAGATCCGTGGCG
ACAAGTGCTGCTGGCGGACAGGCGCTGGAGCGGCGAGTTGTTGAAGCCGCTTGGCCTGGAAGTCCCGTGGTACCGGTG
AAAGGTCAGATGATCCTCTACAAGTGCAGGCGGATTTCTGCCGCGCATGGTCTGGCCAAGGGGCGCTACGCGATTCC
GCGGCGGACAGGCCACATCCTGATCGGCAGCACCTTGAACATTGCGGCTTCGACAAGACGCCGACCGACGAGGCGCTGG
AAAGCCTCAGGGCGTCTGCGGCAGAACTGTTGCCGGAAGTGGCGGACATGCAGCCGGTGGCCACTGGGCGAGGTTGCGC
CCGGGCTCTCCGAAGGCATCCCCATATATCGGTCCGCTGCTGGCTTCGACGGGCTCTGGCTGAATACGGGCGACTACCG
CAACGGTCTGGTCTGGCACCGGCGTCTGCGGCTGCTGGCGGATCTCATGAGCGGGCGGGAACCGATCATCGACCCGG
CCCCCTACGCCCCGGCTGGTCTGAGGAGCGAAACCAAAGGCCTGTCTTCGGACAGGCCTTTTCACTTTTCAGTC
GATGCCACGCTTTTTTCAGGCGGTAGCGCATCGAGCGGAACGTGAGGCCAGGCCAGGCGCTGGGCCGCGGCGGTGCCGTTCCAGC
GGGTCTCCTCGAGTGCCTGCATGA

>ORF32530 (SEQ ID NO:364)

AAAGGCCTGTCCGAAGACAGGCCTTTTGGTTTTCGCTCCTCAGAGGCGACCAGCCGGGGCGTAGGGGGCCGGGTGATGA
TCGGTTCCCGCCCGCTCATGAGATCCGCCAGCAGACGGCAGCAGCCGGTGCCAGGACCAGCCGTTGCGGTAGTGCCCCG
GTATTCAGCCAGAGCCCGTCGAAGCCAGGCACCGGACCGATATAGGGATGCCTTCGGGAGAGCCCGGCGCAACCTGC
CCAGTGGGCCACCGCTGCATGTCCGCCAGTTCGGCAACAGTTCGCCGAGACGCCCTGAGGCTTTCCAGCGCCTCGT
CGGTGCGGCTCTTGTGAAGCCCGAATGTTCCAAGGTGCTGCCGATCAGGATGTGGCCGTCGCGCCGCGGAATCGCGTAG
CGCCCCCTGGCCAGCACCATGCGCGGACAGAAATCCGCCGCGCACTGTAGAGGATCATCTGACCTTTACCGGTACCA
GGGCGATTCCAGGCCAAGCGGCTTCAACAACCTCGCCGCTCCAGGCGCCTGCCGCCAGCAGCACCTTGTGCCACGGATCT
CGCCACGCGAGGTGCGCACGCCGACCACTCGATCGCGCTCGCGCAACCAGCCGCGCACCTCCGTCTGTTTCATGCAACTCG
AGATTGGCGAATTGTTGCAAGGATGCCCGCAATGA

>ORF33705c (SEQ ID NO:366)

GTGATATTTCTCTGTTCTTGGCAAATCGGTAGGAGCCCTGTGGTGAGTAGAGATGTAGTAGTGGTAGGCGCTGGCGTCAT
CGGCCTGTTGACCGCCCGGAGCTGGCGCTCGCCGACTGCGGGTGACCTGGTGGAGCGGGGCGAGAGTGGGCGTGAGG
CATCCTGGGCGGAGGCGGGATCGTCTCGCCGCTCTATCCGTGGCGCTACAGCCCGGCGGTGACCGCCCTGGCGCACTGG
TCGAGGACTTCTACCCGGCCCTGGGGCAGCGTTTGTCTGACGAGACCGGGCTCGATCCCGAGGTCCATACCGTTGGCCT
GTACTGGCTGGACCTGGACGACAGACCGAGGCACTGCAGTGGGCACGCAACCACACCCGGCCGTTGAAGGAAGTGCCGA
TCGAGGAGGCTACGCGGCGGTGCCCGGCTGGGCGCAGGCTTCCAGCGGGCGGTCTACATGTGCGGCGTGCCCAATGTG
CGCAATCCTCGCCTGGCGCGCTCATTGCGGGCATCCCTGCAACAATTGCGCAATCTCGAGTTGCATGAACAGACGGAGGT
GCGCGGCTGGTTGCGCGACGGCGATCGAGTGGTGGCGTGGCGACCTCGCGTGGCGAGATCCGTGGCGACAAGGTGCTGC
TGGCGGACAGGCGCTGGAGCGGCGAGTTGTTGAAGCCGCTTGGCCTGGAAGTGGCGTGGTACCGGTGAAAGGTGAGATG
ATCCTCTACAAGTGCAGGCGGATTTCTGCCGCGCATGGTGTGGCCAAGGGGCGCTACCGGATTCCGCGGCGCGACGG
CCACATCCTGATCGGCAGCACCTTGGAACTTCGGGCTTCGACAAGACGCCGACCGAGGCGCTGGAAGCCTCAGGG
CGTCTGCGGCAGAACTGTTGCCGGAAGTGGCGGACATGCAGCCGGTGGCCACTGGGCGAGGTTGCGCCCGGGCTCTCCC
GAAGGCATCCCTATATCGGTCCGGTGCCTGGCTTCGACGGGCTCTGGCTGAATACGGGCGACTACCGCAACGGGCTGGT
CCTGGCACCGGCGTCTGCGGCTGCTGGCGGATCTCATGAGCGGGCGGGAACCGATCATCGACCCGGCCCCCTACGCCC
CGGCTGGTCGCTCTGA

Fig. 3-31

>ORF32832 (SEQ ID NO:368)

GGCTTTCCAGCGCTCGTCGGTCGGCGTCTTGTGCGAAGCCCGAATGTTCCAAGGTGCTGCCGATCAGGATGTGGCCGTCG
CGCCGCGGAATCGCGTAGCGCCCTTGGCCAGCACCATGCGCGGCAGGAAATCCGCCGCGCACTTGTAGAGGATCATCTG
ACCTTTTACCGGTACCACGGGCAGTTCCAGGCCAAGCGGCTTCAACAACCTCGCCGCTCAGGCGCCTGCCGCCAGCAGCA
CCTTGTGCGCACGGATCTCGCCACGCGAGGTCGCCACGCCGACCACTCGATCGCCGTCGCGCAACCAGCCGCGCACCTCC
GTCTGTTTCAATCGAATCGAGATTGGCGAATTGTTGAGGGATGCCCCGAATGAGCGCGCCAGGCGAGGATTGCGCACATT
GGCCACGCCCGACATGTAGACCGCCCGCTGGAAGCCTGCGCCAGCCCGGGCACCGCCGCTAGGCCTCCTCGATCGGCA
CTTCCTTCAACGCGCGGGTGTGGTTGCGTGCCTGCGAGTGCCTCGGTCTGGTCTGAGGTCCAGGTCAGCCAGTACAGGCCA
ACGGTATGACCTCGGGATCGAGCCCGGTCTCGTCGAGCAAACGCTGCCCCAGGGCCGGGTAGAAGTCTGCGACCAAGTG
CGCCAGGGCGGTACCGCCGGGTGTAGCGCCACGGATAGAGCGGCGAGACGATCCCGCCTCCCGCCAGGATGCCTCAC
GCCCCACTCTCGCCCCGCTCCACCAGGGTCACCCGAGTCCGGCGAGCGCCAGCTCCCGGGCGGTCAACAGGCCGATGA

>ORF33547c (SEQ ID NO:370)

GGCATCTGGGCGGGAGGCGGGATCGTCTCGCCGCTCTATCCGTGGCGCTACAGCCCGGGGTGACCGCCCTGGCGCACT
GGTGCAGGACTTCTACCCGGCCTGGGGCAGCGTTTGTCTGACGAGACCGGGCTCGATCCCGAGGTCCATACCGTTGGC
CTGTACTGGCTGGACCTGGACGACCAAGGAGGCACTGCAGTGGGCAACCAACACCCGGCGGTGAAGGAAGTGCC
GATCGAGGAGGCTACGCGCGGTGCGCGGGTGGGGCAGGCTTCCAGCGGGCGGTCTACATGTCGGGCGTGGCCAATG
TGCGCAATCTCGCTGGCGCGCTCATTGCGGGCATCCCTGCAACAATTGCGCAATCTCGAGTTGCATGA

>ORF33205 (SEQ ID NO:372)

GCGCGCCAGGCGAGGATTGCGCACATTGGCCACGCCCGACATGTAGACCGCCGCTGGAAGCCTGCGCCAGCCCGGGCA
CCGCCGCTAGGCCTCCTCGATCGGCACTTCTTCAACGGCCGGGTGTGGTTGCGTGCCCACTGCAGTGCCTCGGTCTGG
TCGTCCAGGTCCAGCCAGTACAGGCCAACGGTATGGACCTCGGGATCGAGCCCGGTCTCGTCGAGCAAACGCTGCCCCAG
GGCCGGGTAGAAGTCTGCGACCAAGTGCGCCAGGGCGGTACCGCCGGGTGTAGCGCCACGGATAGAGCGGCGAGACGA
TCCCGCCTCCCGCCAGGATGCCTCACGCCCACTCTCGCCCCGCTCCACCAGGGTCACCCGAGTCCGGCGAGCGCCAGC
TCCCGGGCGGTCAACAGGCCGATGACGCCAGCGCTACCACTACTACATCTCTACTACCAACAGGGCTCTACCGATTG
CCAGGAACAGAGAAATATCACTCAAAGGGATCAGATGCTGACGAATTGCTTCAACGAACTCAGTCGAATCTAGTCC
CGGTGAAAAGCCCATCATACCCGAGAGGTATTATCCCATGA

>ORF33512 (SEQ ID NO:374)

AGCGGCGAGACGATCCCGCCTCCCGCCAGGATGCCTCACGCCCACTCTCGCCCCGCTCCACCAGGGTCACCCGCAGTCC
GGCGAGCGCCAGTCCCGGGCGGTCAACAGGCCGATGACGCCAGCGCTACCACTACTACATCTCTACTACCAACAGGGC
TCCTACCGATTGTCAGGAACAGAGAAATATCACTCAAAGGGATCAGATGCTGACGAATTGCTTCAACGAACTCAG
TCGAATCTAGTCCCGGTGAAAAGCCCATCATACCCGAGAGGTATTATCCCATGAAATCGAGTGGTTTGAATTTGGTGG
AACTATCGATAGTCTATCGATCCTTGCATAGGCGTGACAATTGCGCTGCCACCCTCCCGACAGAATGAAGCGGGAC
ATTAG

>ORF33771 (SEQ ID NO:376)

AAAGCCCATCATACCCGAGAGGTATTATCCCATGAAATCGAGTGGTTTGAATTTGGTGGAACTATCGATAGTCTTATC
GATCCTTGCGATAGGCGTGACAATTGCGCTGCCACCCTCCCGACAGAATGAAGCGGGACATTAGCCGTGATATTGGTG
ACAGCCTGACTAGTCATGTGATGGCTGCGCGGGCTAGCAGCATAAGAACGGCGTGATCATCGAGGTGTGCGGTAGCGGT
GACGGCAGTACCTGCAGCGAGGAATGGCATCTCGGTGGTTAGCCGTAACGACAGGAGCCAAAGATACTGGCCCGGCA
TGAAAATACGAGTCGCACCGATATTCAATTGGCGGGGCTTCGACAAGCGACTGCGCTACCTGCCTAATGGCACCAGCCCTA
CAGGTAAACGGGCGTTTCTTGAATGTAAGGACGATCGCATCGAGTGGCAATTGGTGTCTCAATCGGCAAGGCCGCTCAGG
GTGGCGGGAAAGAGCGAAAATAAAAAGCTCTCTTACCTGTGCTCCAGGCGGTGA

>ORF34385c (SEQ ID NO:378)

TGGAGAGCGCATTGTCCCTGTAGCAGAGACAGCCGGAGCGGAGAGTGGGATGACTGGCAAACGGTATGTGAAACAGTTCT
CTCACCGCCTGGAGCACAGGTAAGAGAGCTTTTTATTTTCGCTCTTTCCCGCCACCCTGAGGCGGCCTTGCCGATTGAGC
ACCAATTGCCACTCGATGCGATCGTCTTACATTGCAAGAAACGCCCGTTACCTGTAGGGTGGTGCCATTAGGCAGGTA
GCGCAGTCGCTTGTGCAAGCCCCGCCAATGAATATCGGTGCGACTCGTATTTTCATGCCGGGCCAGTATCTGTTGGCTCC
TGTCGTTACGGCTGAACCAGCCGAGATGCCATTCTCGTGCAGGTACTGCCGTACCGCTACCGCACACCTCGATGATC
ACGCCGTTCTGTATGCTGCTAGCCCGCGCAGCCATCACATGACTAGTCAGGCTGTACCAATATCACGGCTAATGTCCCG
CTTCATTCTGTGCGGGAGGGTGGGCAGCGCAATTGTACGCCTATCGCAAGGATCGATAG

Fig. 3-32

>ORF33988 (SEQ ID NO:380)

TCATCGAGGTGTGCGGTAGCGGTGACGGCAGTACCTGCAGCGAGGAATGGCATCTCGGCTGGTTCAGCCGTAACGACAGG
AGCCAACAGATACTGGCCCGGCATGAAAATACGAGTCGCACCGATATTCATTGGCGGGGCTTCGACAAGCGACTGCGCTA
CCTGCCTAATGGCACCAGCCCTACAGGTAACGGGCGTTTCTTCGAATGTAAGGACGATCGCATCGAGTGGCAATTGGTGC
TCAATCGGCAAGGCCGCTCAGGGTGGCGGAAAGAGCGAAAATAAAAAGCTCTCTTACCTGTGCTCCAGGCGGTGAGAG
AACTGTTTCACATACCGTTTGCCAGTCATCCCACTCTCCGCTCCGGCTGTCTCTGCTACAGGGACAATGCGCTCTCCACT
AG

>ORF34274 (SEQ ID NO:382)

AAAGCTCTCTTACCTGTGCTCCAGGCGGTGAGAGAACTGTTTCACATACCGTTTGCCAGTCATCCCACTCTCCGCTCCGG
CTGTCTCTGCTACAGGGACAATGCGCTCTCCACTAGGCAAGATTATCTGGCCCTTTTCTTGTGGAGTACTGCATGCGCT
CTATTTGTGCGCAGCGCCGGCTTTTCCCTGATCGAGTTGATGATGGTGTGGTTCTGGTGCCTATATTCGCCAGCATTGCC
GTACCCAGTTTCAACGCCTTGATCGAGCGCAACCGAATCCAGACTGCCAGCGAGGAATCTACAGCCTGCTTCAGTACGC
TCGCAGCGAAGCTGTAACCGTCATGCCAATGTGAGCATCAGGGCGACGAGAACAATGACTGGGCAAAAGGCCTGGAAA
TCATCAGCGGCGGACACCGTGCAAAAGCACCAAGGTTTCCAGCAGGTCTCGCTATCCGCCAGCAGTGGCACTGCGGAG
CTGACCTTCAACGCTACCGGCACACTTAGCAACCAGGCTGCAACATTGACATAAAGGTCTGCTTCGCCGGTGACAAAAG
TACAGGACGTCTGCTTACCGTTAGCCCACTGGACGCGTGATCCTGTACCCATCTTCAAAGCAACCGGACAGCTGTAAC
GA

>ORF34726c (SEQ ID NO:384)

CGAGACCTGCTGGAAACCTTGGTGCTTTTGCACGGTGGTTCGCGCCGCTGATGATTTCCAGGCCTTTTGCCCAGTCATTGT
TCTGCGTCGCCCTGATGCTCACATTGGCATGACGGTTTACAGCTTCGCTGCGAGCGTACTGAAGCAGGCTGTAGAGTTCC
TCGCTGGCAGTCTGGATTGCGTTGCGCTCGATCAAGGCGTTGAACTGGGTACGGCAATGCTGGCGAATATGGCGACCAG
AACCAACACCATCATCAACTCGATCAGGGAAAAGCCGGCGCTGCGACAAATAGAGCGCATGCAGTACTCCACAAGGAAAA
GGGCCAGATAATCTTGCCTAGTGGAGAGCGATTGTCCCTGTAGCAGAGACAGCCGGAGCGGAGAGTGGGATGACTGGCA
AACGGTATGTGAAACAGTTCTCTCACCGCTGGAGCACAGGTAA

>ORF34916 (SEQ ID NO:386)

GGAAAGCCCATGTCTCGAGAAACGGGTTTCAGCATGATCGAAGTACTGGTTGCTCTGGTGCTGATCAGCATTGGCGTACT
GGGCATGGTTGCCATGCAAGGGCGCACGATCCAGTACACGAGGAGTCGGTACAACGCAATGCCGAGCAATGCTTGCTA
GCGACCTGATGGAATAATGCGTGCGGACCCAGATGCCGTACTCAATCTACGCGCCCACTACGCGAAGACTCGGTCTAC
TACAAGGCCAAGGGCAGCGACTTTCCCGCAGCCCCAGCGCGCTGCGCGCCATTGCCAGCAGATGCTAAGGAACGTCTCGG
CTGCTGGGCCCCAACAGGCCTCGAAAGACTTGCCGGGAGCCTCCGCACTCTTGAATAGCCAATTCTACATTTGTCGAGCC
CAACCCCGGTACCTGCGACAACACCAAAGGCTCGGCCATCGAAATCCAGGTTGCTGCGAGCCATGGATGGAGCGTGT
TTCAACGCCTCTGACTCCACCTTGTGCACCTACAGCGTCCGCTCCGAATTGTGA

>ORF35464c (SEQ ID NO:388)

AGAGCATGCTTGTCTCACAATTCGAGCGGACGCTGTAGGTGCACAAGGTGGAGTCAGAGGCGTTGAAACACGCTCCAT
CCATGGCTCGCCAGGCAACCTGGATTTCGATGGCCGAGCCTTTGGTGTGTGTCGAGGTACCCGGGGTTGGGCTGCGACAA
ATGTAGAATTGGCTATTCAAGAGTGGGAGGCTCCCGGCAAGTCTTTCGAGGCCTGTTGGGCCCAGCAGCCGAGACGTTT
CTTAGCATCTGCTGGCAATGGCGCGCAGCGCTGGGGCTGCGGGAAGTCTGCTGCCCTTGGCCTTGTAGTAGACCGAGT
CTTCGCGTAG

>ORF35289 (SEQ ID NO:390)

ATAGCCAATTCTACATTTGTGCGAGCCCAACCCCGGGTACCTGCGACAACACCAAAGGCTCGGCCATCGAAATCCAGGTT
GCCTGGCGAGCCATGGATGGAGCGTGTTCACGCCTCTGACTCCACCTTGTGCACCTACAGCGTCCGCTCCGAATTGTG
AGAACAAAGCATGCTCTTCAGCAAAATGCAGAAAGGCTATCGATGGTAGAACTGCTCGTGGCACTCGCTATAAGCAGCTT
CCTGATCCTGGGGATCAGCCAGATCTACATCGACAACAAACGCAACTATCTTTCCAGCAAGGCCAGGCCGGAACAGG
AAATAG

Fig. 3-33

>ORF35410 (SEQ ID NO:392)

CTCCACCTTGTGCACCTACAGCGTCCGCTCCGAATTGTGAGAAACAAGCATGCTCTTCAGCAAAATGCAGAAAGGCCTATC
GATGGTAGAACTGCTCGTGGCACTCGCTATAAGCAGCTTCCTGATCCTGGGGATCAGCCAGATCTACATCGACAACAAAC
GCAACTATCTTTCCAGCAAGGCCAGGCCGGCAACCAGGAAAATAGCCGCTTCGTTCTTATGCTGCTGCAGCAACAACTG
GATAAGACAGCCTATCGTCGCCCTCACGACGACAACATGGAGAATGCTTCAAATCCGCGACATTCAATGGCTGTCGTGC
ATTTGTGGCTGGCGAGACTATCGCTGCGGCACTGCCCTCAAGGCGGGTGAGTACGGTGTCTGCTTGGCGCTATCAACCCG
CCTACAAAGGGGAGCATGATTGCCCTCGGTAATGAAATTACCGGAGTTCGGGAAAAGCCCTTCACAAATACTCCCCCTGTC
GTCGTTGCGCTGGTCTACCTACCGAGCGCCGGTACCCTGAGTTGCAGTCGTCCCGATATCGCCAGTCGAAATCGGGAGA
ATTGGTCAGTGGTCTACAGACTTCGCTTGGGAGCGGGGGTCCGGCCAGCAGATCGTAGCGAACGCAAGTATCCAGCT
TCGTCGCACTACAGGATGTCGCCGGTCTGCTTATCCGAGCATTGCGCTTCTCAATCCTGGCAGGCAGCGACAATACAAGC
CTGCCACAGGAGATGATAGCCAGGCACGCGATCGCTGGATCGTCTTTATCCCGAGAGCAAAAGCCCATCGAGGCCGC
AGACAAAGGCCAGATTTACCAATAGCGCGTGGTAACCAACCATCAGGAATCTCATGCCATGA

>ORF35907c (SEQ ID NO:394)

GTAGACCAGGCGAACGACGACAGGGGAGTATTTGTGAAGGGCTTTTCCGGAACTCCGGTAATTTATTACCGAGGCAAT
CATGCTCCCTTTGTAGGCGGGTTGATAGCGCAAGCAGACACCGTACTCACC CGCCTTGAGGGCAGTTGCCGAGCGATA
GTCTCGCCAGCCACAAATGCACGACAGCCATTGAATGTGCGGGATTGAAAGCATTCTCCATGTTGTCGTCTGAAGGCG
ACGATAGGCTGTCTTATCCAGTTGTTGCTGCAGCAGCATAAGAACGAAGCGGCTATTTTCCTGGTTGCCGGCCTGGCCTT
GCTGGAAGAGATAGTTGCGTTTGTGTCGATGTAGATCTGGCTGATCCCGAGGATCAGGAAGCTGCTTATAGCGAGTGCC
ACGAGCAGTTCTACCATCGATAG

>ORF35534 (SEQ ID NO:396)

TCCTGGGGATCAGCCAGATCTACATCGACAACAAACGCAACTATCTTTTCCAGCAAGGCCAGGCCGGCAACCAGGAAAAT
AGCCGCTTCGTTCTTATGCTGCTGCAGCAACAACTGGATAAGACAGCCTATCGTCGCCCTCACGACGACAACATGGAGAA
TGCTTTCAAATCCGCGACATTCAATGGCTGTCTGTCATTTGTGGCTGGCGAGACTATCGTGGCGCACTGCCCTCAAGG
CGGGTGAGTACGGTGTCTGCTTGGCTATCAACCCGCTACAAAGGGGAGCATGATTGCCCTCGGTAATGAAATTACCGGA
GTTCCGGAAAAGCCCTTCACAAATACTCCCCCTGTCGTGCTTGCCTGGTCTACCTACCGAGCGCCGGTACCCTGA

>ORF35930 (SEQ ID NO:398)

GTTGAGTCGTCCGATATCGCCAGTCGAAATCGGGAGAATTGGTCAGTGGTCTCACAGACTTCCGCTTGGAAAGCGGGG
GTCGGGCCAGCAGATCGTAGCGAACGCAAGTATCCAGCTTCGTGCACTACAGGATGTGCGCGGTGCTCTATCCGAGC
ATTGCGCTTCTCAATCCTGGCAGGCAGCGACAATACAAGCCTGCGCACAGGAGATGATAGCCAGGCACGCGATCGCTGGA
TCGTCTTTTATCCCGAGAGCAAAAGCGCCATCGAGGCCGAGACAAAGGCCAGATTTACCAAAATAG

>ORF36246 (SEQ ID NO:400)

CCAAACCATCAGGAATCTCATGCCATGACCCTGCGCCATACCTCTCGACAGCAGGGATCCACGTTGTTGATCTCGCTGGT
TATCTTGTGATGATCACGCTCCTCGCCGTTTCCAACATGCGCGAGGTGTCACTGGAAAGCCGTATCACC GGCAATCTCA
TCGAACAGAAGCGCTGCGCAATGCGGGCGAAGCTGGGCTACGCGAAGGTGAACGACGCTTTTCAATACCATCAAGCCC
CCAGAGGTGCGCAGCGGATGCGCCGATAGCAATGTCAAACGGCCTTGCCATACTGAACCTGAGTGCCCTCTCCGTACCCCG
AGATGACGTGCACAACAATCCGGTGGCAGCCCTGAACGGCAAGACAGATAACGCCAATTCACGTGTCTGGATGCCCTACC
GAGGCAGCGATCTGAATAACCTACGCAGATCGACAAAGACCGCGCAGTCACCTGGCAGACCATCACGGTGCCCGCTGGC
GAACAGAACAACGAAGCGGAAAATCCCGAGTACGGCAACATGATGCGCGGGGTGCGCACGTTCTACTACGAAAACCAACAG
CCGCGCCCTCAACAAGGCGGGCGGAGAGACTGTTCTACAGGCCGTTTCATGCACGCTGTATACCAACTGA

>ORF26640c (SEQ ID NO:402)

GGCATCCAGACACGTGAATTGGCGTTATCTGTCTTGCCGTTTCAGGGCTGCCACCGGATTGTTGTGCACGTCATCTCGGGG
TACGGAGAGGGCACTCAGGTTAGTATGCAAGGCCGTTTGCATTGCTATCGGGCGCATCCGCTGCCGACCTCTGGGGGCT
TGATGGTATTGAAAAAGCGTCTTACCTTCGCGTAGCCAGCTTCGCCCGCATTGCGCAGGCGCTTCTGTTGATGAGA
TTGCCGGTGATACGGCTTTCAGTGACACCTCGCGCATGTTGGAAACGGCGAGGAGCGTGATCATCAACAAGATAACCAG
CGAGATCAACAACGTGGATCCCTGCTGTCGAGAGGTATGGCGCAGGGTCATGGCATGA

Fig. 3-34

>ORF36769 (SEQ ID NO:404)

TGGCGGGGTCGGCACGTTCTACTACGAAACCAACAGCCGCGCCCTCAACAAGGCGGGCGGAGAGACTGTTCTACAGGCC
 GTTCATGCACGCCTGTATACCAACTGACTGGAGCCAGCGCATGATCCACCAGATTACCCGCGCAGGAAAAAGCCTGCTGG
 CTGCAGGTTGCACCCTGAGCATCCTGTTCCGCTCTGACAGTTATGCCGCCACGGCCCTGAATGTCAGCCAGCAACCCCTG
 TTCCTAACCCAGGGCGTTGCTCCCAACCTGCTGTTCACTCTAGATGACTCAGGCAGTATGGCCTGGGCTTACGTGCCCGA
 CGGTATTAGCGGGAATAGCGGCAGAGCGGGACGTTCCAGCGATTACAACGCACTGTACTACAACCCCGATTATGCTTACC
 AAGTGCCCAAGAAATTGACACTGTGAGGCGATCAGATCATCGTTCCGACTATCCAGTGCCACGCTTCACAGCAGCCTGG
 CAGGATGGCTACGCCCAGGCTCCACCACCAACCTGAGCAATAACTATCGCCCTCAATGGGGAACCGGCTGGCTTGGTTG
 CATCGATAGCAGCTGCAATACCGGGAGAGCTTATTACTATACTTATAAGGTAAGCGCTAGCTGCCCTGCACAGCCGGTGA
 GCAGCTCCAACCTCCTGTTATACCTACAATGCTCTTCTACCAGTCAGGAAAGCAACTTTGCGATATGGTACTCCTACTAT
 CGCAACCGCATCCTGGCCACAAAGACCGCTGCCAACCTGGCCTTTTACAGCCTGCCGGAACCGTGGCTCTCACTTGGGG
 GGCCCTGAACACCTGTAGCATCGGCGCCAACAGCAGAAGCTGCCAAAACAATGCCCTGCTCCAATTCAACAAGCAGCACA
 AAATCAATTTCTTCAATTGGCTGGCGAACAGCCCGGCCAGCGGCGGTACTCCTCTGCATGCGGCTCTTGACCGAGCCGGA
 CGCTTCTTGCAAACCAACGGCACAGCTTATACCACGAAGACGGAAAGACATATTCCTGCCGGGCCAGCTATCACATCAT
 GATGACCGACGGTATCTGGAACGGTCGGAACGTACCCCCGGCAATCTCGACAACCAGAACCAGACCTTTCTGATAGCA
 CCTCTATAGGCCACAGCCCCCTTATGCCGACAGCAATGCCAGCTCATTGGCTGACCTGGCTTTCAAATACTGGACCACA
 GACTTACGTCCCAGCATCGACAATGACCTGAAGCCTTTTATGGCCTACAAGAGTGGGACGATTCCAAGGATTACTGGGA
 CCTCGCAACAACCCAGCCACTTGGCAACACATGGTCAACTTTACCGTTGGCCTAGGTCTTTCTATTGCTCACATTGA
 ACTCTGCACCAACTTGGACAGGCAGCACCTTTGGCAACTACGAGGAGTTGATGGCTGGAAGCAAGGCTTGGCCAGCGTC
 GATAACGACGCCGCAACCGGTAACGTCTACGACCTCTGGCATGCAGCTATCAACTCTCGTGGAGACTTCTTTAGCGCGGA
 ATCACC GGACTCTCTGGTTCAGGCTTCAATAAGATCCTGACACGGATTTCCGAGCGCAACACCTCCTCTCCAAACCAG
 CAATGACTTCCGCGCTGCAGGATGACGGAACCGGCGACAAGCTGATCCGCTACAGCTACCAGTCCAGCTTTGCCAGTGAC
 AAGAAGTGGGCGGGCGACCTTATACGTTACAAGGTGGAGTCGACTTCCACCGGTTGACCAAAACCCAGGAATGGAGCGC
 CGGCGCACTGCTGGACAACCGAGCTCCCGCTACCCGTAATATTTACATCGCCAGCAATAGCGGAACCAACCGCCTTAAGC
 CTTTTCATGAGCAATATTGAGGGAAGTCAGTTAGCCACTTGGCTGAACCGCAACCCGGACAAGGACAATCAGGCCGAC
 ACCAAAGGAGCACAGCGGTGCACTTCCGTGGCCAGCAGAATATGGATGGATTCCGGCAACGACAGGCGGTGTTAGG
 GGACATCGTGCACTCGTCTCCAGCCGTGGTGGACCGGCCCAATACCTCACTTATCTGGCCAACCCCATCGAACCAGCG
 GCGACTACGGCACATTCAAGACAGAGGCAGACCAGCGCAGCCCTAGAGTTTATGTTGGATCCAACGATGGCATGTTGCAT
 GGTTTCAACATCAAAACCGGCGTGAAGAGTTCGCTTTCATCCCTACAGCAGTATTCGAAAAGCTTAACAAGCTTACCGG
 CATCAGCTACCAGGGCGGTGCCACCAATATTTCTGTCGACGCTACACCGGTGTCAGCGATGCCTTTTTTCGATGGAGCTT
 GGCACACTGTTCTGATCGGAACGCTTGGTGGTGGAGTTCGCGGCTGTTGCGCACTCGATGTAACCAAGCCGGACGATGTC
 AAGCTGCTTTGGGAATACGATAGCAGTACCGACTCGGACCTTGGTTACACCTTCTCCAAACCTACCGTAGCCAGACTGCA
 CAGCGGACAATGGGCAGTAGTTACCGGCAACGGCTATGGAAGCGATAATGACAAGGCAGCTTTACTGCTGATTGATTGA
 AAAAGGGAACGCTGATCAAGAAGCTGGAAGTCCAAGCGAGCGCGGAATAGCCAATGGCCTATCGACGCCTCGCCTGGCT
 GATAACAACAGCGATGGCATTGCTGACTACGCCTATGCTGGCGATCTGCAGGGAATATCTGGCGCTTCGATTGATCGG
 CAATACCCGCAACGACGACCCAGACACAATACCTCTATCAATCCCTTCAAGCCCGGAGATGTAGATCCTTCTGCTTTCA
 GAGTATCGTTCAGCGGCGCCCGCTTTTCCGTGCTCGCGCGACAACAATACTCGTCAGCCCATCACGGCTCCGCTACC
 TTGGTACGCCATCCTAGCCGTAAGGGCTACATCGTCATCGTAGGTACAGGAAAATACTTCGAGGACGATGACGCTCAGGC
 CGATACAGCCGAGCCATGACGCTCTATGGTATCTGGGATCGCCAGACCAAGGGCGAAAGCGCAACAGTACCCCAACCA
 TCGACCGCAACGCCCTCACAGCCCAACCATGACAACAGAGGCGAACTCCACATTCCGTAGCGTGAACAGGAATATTCGG
 CTTATTAGCCAAAACCCGGTGAAGTGGTACAAAGACGGAGCAACCGGTACCGGAACTCGGATGTGGCTAGCTATGGCTG
 GCGACTGAATCTGGAGGTCAATAGCAGCAAGAAAGCGAAATGATGATCGAAGATATGTTGCTGCGGCGCAAGTGCTTC
 TATTGCAGACCTTGACACCGAACGACGACCCCTTGTGACAGCGGCTCTACCAGCTGGACCTACGGCCTCAATCCATATACT
 GGCGGACGTACAGTTTACCCTCTTCGATCTCAAACGTGCGGGTATAGTGGACTCTGGCTCGGATTACAACGGCTCGGT
 CGTATCCGCTTCCAACAGGATGGAAGTGGCTTGGCCATTACCCAGAACGAACAGCGTCAATCCGAGGCTTGCAGTG
 GTGATGAGTGCATCATCTTCAACCCAGCGACAAGAGTAACGGACGACAACCTGGCGGTCGTCAGGAGAAATGA

Fig. 3-35

>ORF37932c (SEQ ID NO:406)

GCTGGCATTGCTGTCCGCATAAGGGGGCTGTGGCCTATAGAGGGTGCTATCAGGAAAGGTCTGGTTCTGGTTGTCGAGAT
TGCCGGGGGTGACGTTCCGACCGTTCCAGATACCGTCGGTCATCATGATGTGATAGCTGGCCCGGCAGGAATATGTCTTT
CCGTCTTCGGTGGTATAAGCTGTGCCGTTGGTTTGCAAGAAGCGTCCGGCTCGGTCAAGAGCCGCATGCAGAGGAGTACC
GCCGCTGGCCGGGCTGTTGCCAGCCAATTGAAGAAATTGATTTTGTGCTGCTTGTGAATTGGAGCAGGGCATTGTTTT
GGCAGCTTCTGCTGTTGGCGCCGATGCTACAGGTGTTCAAGGGCCCCCAAGTGAGACGCACGTTTTCCGGCAGGCTGTAA
AAGGCCAGGTTGGCAGCGGCTTTTGTGGCCAGGATGCGGTTGCGATAGTAGGAGTACCATATCGCAAAGTTGCTTTCCTG
ACTGGTAGGAAGAGCATTGTAGGTATAACAGGAGTTGGAGTGCTCACC GGCTGTGCAGGGCAGCTAGCGCTTACCTTAT
AAGTATAGTAATAAGCTCTCCCGGTATTGCAGCTGCTATCGATGCAACCAAGCCAGCCGGTTCCCCATTGAGGGCGATAG
TTATTGCTCAGGTTGGTGGTGGAGCCTTGGGCGTAGCCATCCTGCCAGGCTGCTGTGAAGCGTGGCACTGGATAGTCGGA
AACGATGATCTGATCGCCTGA

>ORF38640c (SEQ ID NO:408)

CTGACTTCCCTCAATATTGCTCCATGTGAAAGGCTTAAGGCGGTTGGTTCCGCTATTGCTGGCGATGTAAATATTACGGG
TAGCGGGAGCTCGGTTGTCCAGCAGTGCGCCGGCGCTCCATTCTGGGTTTTGGTGAACCGGTGGAAGTCGACTCCACC
TTGTAACGTATAAGGTCGCCCGCCAGTTCTTGTCACTGGCAAAGCTGGACTGGTAGCTGTAGCGGATCAGCTTGTCCGC
GGTTCCGTATCCTGCAGCGCGGAAGTCATTGCTGGTTTGGAGGAGGAGGTGTTGCGCTCGGAAATCCGTGTGAGGATCT
TATTGAAAGCCTGAACCAGAGAGTCCGGTGA

>ORF39309c (SEQ ID NO:410)

AGCTGCCTTGTATTATCGCTTCCATAGCCGTTGCCGTAACACTACTGCCATTGTCCGCTGTGCAGTCTGGCTACGGTAG
GTTTGGAGAAGGTGTAACCAAGGTCCGAGTCGGTACTGCTATCGTATTCCCAAAGCAGCTTGACATCGTCCGGCTTGGTT
ACATCGAGTGCGAACAGGCCGCGACCTCCAGCACCAGCGTTCCGATCAGAACAGTGTGCCAAGCTCCATCGAAAAAGGC
ATCGCTGACGACCGGTGTAGCGTCGACGAAATATTGGTGGGCACCGCCCTGGTAGCTGATGCCGGTAAGCTTGTAAAGCT
TTTGAATACTGCTGTAGGGATGAAAGCGAACTCTTCCACGCCGGTTTTGATGTTGAAACCATGCAACATGCCATCGTTG
GATCCAACATAAACTCTAGGGCTGCGCTGGTCTGCCTCTGTCTTGAATGTGCCGTAGTCGCCGCTGGGTTGATGGGGTT
GGCCAGATAAGTGAGGTATTGGGCCGGTCCGACCACGGCTGGAGACGAGTGACGATGTCCCCTAA

>ORF38768 (SEQ ID NO:412)

GGGACATCGTGACTCGTCTCCAGCCGTTGGTCCGACCGGCCCAATACCTCACTTATCTGGCCAACCCCATCGAACCCAGC
GGCGACTACGGCACATTCAAGACAGAGGCAGACCAGCGCAGCCCTAGAGTTTATGTTGGATCCAACGATGGCATGTTGCA
TGGTTTCAACATCAAACCGGCGTGGAGAGTTGCTTTTATCCCTACAGCAGTATTCGAAAAGCTTAACAAGCTTACCG
GCATCAGCTACCAGGCGGTGCCACCAATATTTCTGTCGACGCTACACCGGTCGTCAGCGATGCCTTTTTTCGATGGAGCT
TGGCACACTGTTCTGA

>ORF40047c (SEQ ID NO:414)

AAGCACTTGGCCGGCAGCGAACATATCTTCGATCATCATTTGCGCTTTCTTGCTGCTATTGACCTCCAGATTCAGTCGCC
AGCCATAGCTAGCCACATCCGAGTTCGCGGTACCGGTTGCTCCGCTTTTGTACCACTTACC GGTTTTGGCTAATAAGC
CGAATATTCTGTTACGCTACCGAATGTGGAGTTCGCTCTGTTGTATGGTTTGGGCTGTGAGGGCGTTGCGGTCGAT
GGTTGGGGTACTGTTTGCCTTTTCCGCTTGGTCTGGCGATCCCAGATACCATAGAGCGTCATGGCTCGGCTGGTATCGG
CCTGAGCGTCATCGTCTCGAAGTATTTTCTGTACCTACGATGACGATGTAGCCCTTACGGCTAGGATGGCGTACCAAG
GTAGGCGGAGCCGTGATGGGCTGACGAGTATTGTTGTGCGCGCGAGCACGAAAAGCGGGCGCCGCTGAACGATACTCT
GAAAGCAGAAGGATCTACATCTCCGGGCTTGAAGGGATTGATAGAGGTATTTGTGTCTGGGTCGTGTTGCGGGTATTGC
CGATCAAATCGAAGCGCCAGATATTTCCCTGCAGATCGCCAGCATAGGCGTAGTCAGCAATGCCATCGCTGTTGTTATCA
GCCAGGCGAGGCGTCGATAG

>ORF40560c (SEQ ID NO:416)

CCGGCGAGTCCTGTTGTTGGACACGGTTGGGCAAGCGATATGTCTGCCCATCGACTACTACCAGACCGGCGGCAGGATGA
ACATCCTCGACCACGCCACATTCTCGAACGATTCTGTTGGCACTCAAGGCAAAGGTTGGGCAAGCCAGAGCTAGAGCTGC
AAGAGCTGTGGCGAGAAGACGTAAGGGGTTTATGTTTCTTCTCCTCGACGACCCGCGAGGTTTGTGTCCTTACTCTT
GTCGCTGGGGTTGAAGATGATGCACTCATCACCAGTGCAAGCCTCGGATTGACGCTGTTCTGGGTAATGGCCAAGC
CACCTAG

Fig. 3-36

>ORF40238 (SEQ ID NO:418)

GTGGCTTGGCCATTACCCAGAACGAACAGCGTCAATCCGAGGCTTGCCTGGTGATGAGTGCATCATCTTCAACCCAGC
GACAAGAGTAACGGACGACAAACCTGGCGGGTCGTCGAGGAGAAATGAACATGAACCCCTTACGTCTTCTCGCCACAGCT
CTTGACGCTCTAGCTCTGGCTTGGCCAACTTTGCCTTGAGTGCCACGAATACGTTTCGAGAATGTGGGCGTGGTCGAGGA
TGTTTCATCCTGCCGCCGGTCTGGTAGTAGTCGATGGGCAGACATATCGCTTGGCCAAACCGTGTCCAACAACAGGACTCGC
CGGTTCATATTCTTGGTACGTCAGGGACAGACAGTGTCTTTCTCCGGCAAACCTACCAGCGACCTGCCAGAAATCGAGTCG
TTCTACATTATCAAGCAGGCCCCCTCTCGTTCCCTTTCGGATCGGAGCAGCAACAATGAAGTCGAACAGAGGCTTCACTCTC
ATCGAGTTGATGATCGTCGTAGTAATCATCGCTATTCTTGTCTGGTATCGCCTACCCAGCTACGACGAATACGTGAAGCG
CGGGAATCGCACCGAAGGACAGGCATTACTCAGCGAAGCAGCCGCTACTCAAGAGCGCTATTTTTCACAGAACAATACTT
ATATCACTACCCAAGCCGACATCGGCAAGCTGCATATGCGCAACACATCGGGCACCACAGTGAAGTCTCCACAGGCAAA
TACAGCCTTACCGTCGATACGGTAGCCAACGACGAGGTTATCGCTTATCGCTAACAGGCATTCAACGATCTTGATTG
TGGCAACCTGACCTTGACCGCCAACGGCGAGAAAGGCCGGACTGGAAGCAAGAAGAGCGTTGCAGAATGCTGGCGCTAA

>ORF40329 (SEQ ID NO:420)

CGGACGACAAACCTGGCGGGTCGTCGAGGAGAAATGAACATGAACCCCTTACGTCTTCTCGCCACAGCTCTTGACGCTCT
AGCTCTGGCTTGGCCAACTTTGCCTTGAGTGCCACGAATACGTTTCGAGAATGTGGGCGTGGTCGAGGATGTTTCATCCTG
CCGCCGGTCTGGTAGTAGTCGATGGGCAGACATATCGCTTGGCCAAACCGTGTCCAACAACAGGACTCGCCGGTTCATATTC
TTGGTACGTCAGGGACAGACAGTGTCTTTCTCCGGCAAACCTACCAGCGACCTGCCAGAAATCGAGTCGTTCTACATTAT
CAAGCAGGCCCCCTCTCGTTCCCTTTCGGATCGGAGCAGCAACAATGA

>ORF40709c (SEQ ID NO:422)

AGCCTCTGTTGACTTCATTGTTGCTGCTCCGATCCGAAGGGAACGAGAGGGGCTGCTTGATAATGTAGAACGACTCGA
TTTCTGGCAGGTCGCTGGTGTGAGTTTCCGGGAGAAAGACACTGTCTGTCCCTGACGTACCAAGAATATGACCGGCGAGTCC
TGTGTTGGACACGGTTGGGCAAGCGATATGTCTGCCATCGACTACTACAGACCGGCGGAGGATGAACATCCTCGAC
CACGCCACATTCTGAACGTATTCTGTCGACTCAAGGCAAAGGTTGGGCAAGCCAGAGCTAG

>ORF40507 (SEQ ID NO:424)

TCGATGGGCAGACATATCGCTTGGCCAAACCGTGTCCAACAACAGGACTCGCCGGTCATATTCTTGGTACGTCAGGGACAG
ACAGTGTCTTTCTCCGGCAAACCTACCAGCGACCTGCCAGAAATCGAGTCGTTCTACATTATCAAGCAGGCCCCCTCTCGT
TCCCTTCGGATCGGAGCAGCAACAATGAAGTCGAACAGAGGCTTCACTCTCATCGAGTTGATGATCGTCGTAGTAATCAT
CGCTATTCTTGTGTTATCGCCTACCCAGCTACGACGAATACGTGAAGCGCGGGAATCGCACCGAAGGACAGGCATTAC
TCAGCGAAGCAGCCGCTACTCAAGAGCGCTATTTTTCACAGAACAATACTTATATCACTACCCAAGCCGACATCGGCAAG
CTGCATATGCGCAACACATCGGGCACCACAGTGAAGTCTCCACAGGCAAATACAGCCTTACCGTCGATACGGTAGCCAA
CGACGGAGGTTATCGCTTATCGCTAA

>ORF41275c (SEQ ID NO:426)

GTGGGGGGCGTCGGAAGAGCAGGAACCTGGAGGGACGGGAGGAGAACATTACCTTCTCGATGCCAAGGAACTGCGGGTCA
AGGCTTTGTAATCGGAATTTTTCGCGACCTGAAAAGCCCGGCTTATGCCGGGCTTTGCCCTTTTCTTGTCTCGGCGCTT
TAGCGCCAGCATTCTGCAACGCTCTTCTTGTCTCCAGTCCGGCCTTTCTCGCCGTTGGCGGTCAAGGTCAGGTTGCCACA
ATCAAGATCGTTGAATGCCTGGTTAGCGATAAGGCGATAACCTCCGTCGTTGGCTACCGTATCGACGGTAAGGCTGTATT
TGCCTGTGAGGACTTCACTGTGGTGCCGATGTGTTGCCATATGCAGCTTGCCGATGTGCGGCTTGGGTAGTGATATAA
GTATTGTTCTGTGA

>ORF42234c (SEQ ID NO:428)

TCGACGTCCAGCCGGCCTGAACCGTCGGTCGCTGCGCCCTTCCCAAGCGGGAGGGCGGTAGCAAGGTTTATTTCGTCCAA
TCACCGCGTCGCCCACGAGACCGCCATGCAAATCAAACCTCGCCAATCCCCGCGGCTTCTGCGCCGGCGTGGATCGCGCCA
TCGAGATCGTCAACCGTCCCTCGATGTCTTCGGCCCGCGGATCTACGTGCGTCACGAGGTGGTGCAACAACAGTTTCGTC
GTGGACAACCTGCGCCAGCGCGGCGCCATCTTCGTGAGGAACTCGATCAGGTGCCGGAACAGTCATCGTCATCTTCAG
CGCCACGGCGTTCCTCAGCGGTCCGCAAGGAAGCCGAGGGGCGCGGCTGAAGGTTTTCGACGCGACCTGCCCGCTGG
TGACCAAGGTGCACATGGAAGTGGTGCGCTACAGCCGCGACGGCCACGAATCGGTGCTGATCGGGCATGAAGGCCACCCC
GAGGTGGAAGGCACCATGGGCCAGTACGATGCCAGAACGGCGGTGCCATCTACCTGGTGGAGGACGAGGCCGACGTGCG
CGCGCTGGAGGTGCGCAAGCCCAAGCCCTGCACTACGTGACCAGACACCCTGTGATGGACGACACCTCGAAGGTCA
TCGATGCCCTGCGGCCAAGTTCCCGCAGATCCAGGGGCGCGCAAGAACGACATCTGCTATGCCACCCAGAACCGCCAG
GATGCCGTGAAGGAACTGGCCGACCAAGTGCAGATGGTCTTGGTGGTGGGACGCCCCAACAGTTTCAAACCTCAAACCGCCT
GCGCGAAGTCCCGAGCGCATGGGCACGCGGCTTACCTGATCGACGGCGCGGAGGACATGCAACGCGGCTGGTTTCGACG
GTGTGCGTCGCATCGGAATACCGCAGGCGCTCCGCGCGGAAGTGCTGGTGGCGGAGTGATCGCCAGCTACGTGAG
TGGGGGGCGTCGGAAGAGCAGGAACCTGGAGGGACGGGAGGAGAACATTACCTTCTCGATGCCAAGGAACTGCGGGTCAA
GGCTTTGTAA

>ORF41764c (SEQ ID NO:430)

AGGCCACCCCGAGGTGGAAGGCACCATGGGCCAGTACGATGCCAGCAACGGCGGTGCCATCTACCTGGTGGAGGACGAGG
CCGACGTCGCGCGCTGGAGGTGCGCAAGCCCGAAGCCCTGCACTACGTGACCCAGACCACCCTGTGATGGACGACACC
TCGAAGGTCATCGATGCCCTGCGCGCCAAGTTCCCGCAGATCCAGGGGCGCGCAAGAACGACATCTGCTATGCCACCCA
GAACCGCCAGGATGCCGTGAAGGAACTGGCCGACCAGTGGCAGATGGTCTTGGTGGTGGGCGAGCCCCAACAGTTCCAAC
CCAACCGCCTGCGCGAACTCGCCGAGCGCATGGGCACGCCGGCCTACCTGATCGACGGCGCGGAGGACATGCAACGCGGC
TGGTTCGACGGTGTGCGTCGCATCGGAATCACCAGGCGCCTCCGCGCCGGAAGTGTGCTGGTGGCGGAGTGATCGCCCA
GCTACGTGA

>ORF41284 (SEQ ID NO:432)

CTGGGCGATCACTCCGCGCACCAGCACTTCCGGCGCGGAGGCGCCTGCGGTGATTCCGATGCGACGCACACCGTCGAACC
AGCCGCGTTCATGTCTCGGCGCCGTGCGATCAGGTAGGCCGCGGTGCCATGCGCTCGGCGAGTTCGCGCAGGCGGTTG
GAGTTGGAACGTGTTGGGGCTGCCACCACCAGGACCATGTGCACTGGTCGCCAGTTCCCTTCACGGCATCCTGGCGGTT
CTGGGTGGCATAGCAGATGTGTTCTTGGCGGGCCCTGGATCTGCGGGAACCTGGCGCGCAGGGCATCGATGACCTTCG
AGGTGTCGTCCATCGACAGGGTGGTCTGGGTACGTAAGTGCAGGGCTTCGGGCTTGGCGACCTCCAGCGCGGCGACGTG
GCCTCGTCTCCACCAGGTAGATGGCACCAGCGGTTGCTGGCATCGTACTGGCCCATGGTGCCTTCACCTCGGGGTGGC
TTCATGCCGATCAGCACGCATTCTGGCCGTGCGGGCTGTAGCGCACCACTTCCATGTGCACCTTGGTCACAGCGGGC
AGGTGCGTTCGAAAACCTTCAGGCCGCGCCCTCGGCTTCTTGGGACCGCCTGGGAAACCGCGTGGGCGCTGAAGATG
ACGATGACGTTGTCCGCGACCTGATCGAGTTCTCGACGAAGATGGCGCCGCGTGGCGCAGGTTGTCCACGACGAACCT
GTTGTGCACACCTCGTGACGCACGTAGATCGGCGGGCCGAAGACATCGAGGGCACGGTTGACGATCTCGATGGCGCGAT
CCACGCCGCGCAGAAGCCGCGGGGATTGGCGAGTTTGATTTGCATGGCGGTCTCGTGGGCGACGCGGTGATTGGACGAA
TGAACCTTGCTACCGCCCTCCCGCTTGGGAAGGCGCAGCGACCGACGGTTCAGGCCGCTGGACGTCGA

>ORF41598 (SEQ ID NO:434)

CCTTCGAGGTGTCGTCCATCGACAGGGTGGTCTGGGTACGTAGTGCAGGGCTTCGGGCTTGGCGACCTCCAGCGGGCG
ACGTGGGCTCGTCTCCACCAGGTAGATGGCACCAGCGGTTGCTGGCATCGTACTGGCCCATGGTGCCTTCCACCTCGGG
GTGGCCTTCATGCCGATCAGCACGCATTCTGGCGGTGCGGGCTGTAGCGCACCACTTCCATGTGCACCTTGGTCACCA
GCGGGCAGTTCGCGTCGAAAACCTTCAGGCCGCGCCCTCGGCTTCTTGGGACCGCCTGGGAAACCGCGTGGGCGCTG
A

>ORF42172c (SEQ ID NO:436)

CAAGGTTCAATTCGTCCAATCACCGCGTCGCCCACGAGACCGCCATGCAAATCAAACCTCGCCAATCCCCGCGGCTTCTGCG
CCGGCGTGGATCGCGCCATCGAGATCGTCAACCGTCCCTCGATGTCTTCGGCCCGCCGATCTACGTGCGTCACGAGGTG
GTGCACAACAAGTTCTGTCGTGGACAACCTGCGCCAGCGCGGCGCCATCTTCGTGAGGAACTCGATCAGGTGCCGACAA
CGTCATCGTCATCTTCAGCGCCACGGCGTTTCCAGGCGGTCCGCAAGGAAGCCGAGGGGCGCGGCTGAAGGTTTTTCG
ACGCGACCTGCCCCGTGGTGACCAAGGTGCACATGGAAGTGGTGGCTACAGCCGCGACGGCCACGAATGCGTGCTGATC
GGGCATGA

>ORF42233c (SEQ ID NO:151)

CGACGTCCAGCCGGCTGAACCGTCGTCGCTGCGCCCTTCCCAAGCGGGGAGGCGGTAGCAAGGTTCAATTCGTCCAAT
CACCGCGTCGCCACGAGACCGCCATGCAAATCAAACCTCGCCAATCCCCGCGGCTTCTGCGCCGGCGTGGATCGCGCCAT
CGAGATCGTCAACCGTGCCTCGATGTCTTCGGCCCGCGATCTACGTGCGTCACGAGGTGGTGCACAACAAGTTCTGTCG
TGGACAACCTGCGCCAGCGCGGCGCCATCTTCGTGAGGAACTCGATCAGGTGCCGACAACTCATCGTCATCTTCAGC
GCCACGGCGTTTCCAGGCGGTCCGCAAGGAAGCCGAGGGGCGCGCCTGA

Fig. 3-38

>ORF42233c (SEQ ID NO:151)

CGACGTCCAGCCGGCCTGAACCGTCGGTCGCTGCGCCCTTCCCAAGCGGGAGGGCGGTAGCAAGGTTTCATTCGTCCAAT
CACC GCGTCGCCCACGAGACCGCCATGCAAATCAAACTCGCCAATCCCCGCGGCTTCTGCGCCGGCGTGGATCGCGCCAT
CGAGATCGTCAACCGTGCCCTCGATGTCTTCGGCCCGCCGATCTACGTGCGTCACGAGGTGGTGCACAACAAGTTCGTCTG
TGGACAACCTGCGCCAGCGCGGCCCATCTTCGTTCGAGGAACTCGATCAGGTGCCGACAAACGTCATCGTCATCTTCAGC
GCCACGGCGTTTCCCAGGCGGTCCGCAAGGAAGCCGAGGGGCGCGGCCTGA

Fig. 3-39

CGACGTCCAGCCGGCCTGAACCGTCGGTCGCTGCGCCCTTCCCAAGCGGGAGGGCGGTAGCAAGGTTTCATTCGTCCAAT
CACC GCGTCGCCCACGAGACCGCCATGCAAATCAAACTCGCCAATCCCCGCGGCTTCTGCGCCGGCGTGGATCGCGCCAT
CGAGATCGTCAACCGTGCCCTCGATGTCTTCGGCCCGCCGATCTACGTGCGTCACGAGGTGGTGCACAACAAGTTCGTCTG
TGGACAACCTGCGCCAGCGCGGCCCATCTTCGTTCGAGGAACTCGATCAGGTGCCGACAAACGTCATCGTCATCTTCAGC
GCCACGGCGTTTCCCAGGCGGTCCGCAAGGAAGCCGAGGGGCGCGGCCTGA

>ORF2 (SEQ ID NO:3)

SPIQCQGVPGQSEPTGCRGRHCQAPGRRREQHQYRLQRQRHQLRDDRNOQQLGFPQQHPLRRRQRHPAVDEQVVRGGLRR
RLRAARCAGRSASRSATGDRL*

>ORF3 (SEQ ID NO:5)

RRSNAKEYLGNQSLTAAAGAGIAKLLDADENNTSTVFSNGTSFGTTGTNSNSALNSILSGGVSDIRQWMNKLYGEAFAA
VYVQPGARVAVHLDQQLAIDYELKGRKVDYSSGAAHATADLD*

>ORF602c (SEQ ID NO:7)

SAWSFAEASCCGSIGRRSVCLASRSSRPLLPIELVAPRSQTSSMLASPWGSISSLLVEHAARVSAQARPAQRRRRGLVQ
VCCMSGSRVIDLALEFIVDRQLLIEMHCDPRTWLHVDGGEGLPVQLVHPLPDVADAAGEDAVEGRVAVGSGRPEAGA
VAAEDGTGVVLGVQELGNAGPGSRE*

>ORF214 (SEQ ID NO:9)

TSCTGRPSPPTCSQVRGSCISISNWRSTMNSRAARSITALEPLMQQQTWTNPLRLCAGLACALTLAACTSKKEMLP
HGEANMLDVWERGATSSIGNSRGRLLLDARQTLRRPIDPQQDASANDQADYTRTASNEIHSQFKRLPNPDLVMYVFPFLA
GSDPAPVPGYTTVFPFYQVRVQYAMPGERTEDY*

>ORF1242c (SEQ ID NO:11)

SRPGRRTGQSRVFRARRRSSAGLLSMRPGRSASNWDGPRCPRAPVRRMRRANAHPPGASLARRAGTQPRAAGLRTMGR
DRRGVTLRPAWRHSCSRCAEEYPWRPVAPDSAQSLPLRPLRALLNLRERLPVPTAEVCDRAEGFEKSPSIVLRAFARH
GVLDLVEGEHGGVARYRGGAAGQVREHHQVIGIGQSFELTVDLVAGRAGVGLVIRGGILLRIDWAPQRLPGIEEQP
ATAVAYRAGRTSLPDVEHVGLAVGQHLHLAGGARCQGRAGQAGAETKKGVSPLLHERLQSCNRPCGP*

>ORF594 (SEQ ID NO:13)

PGRLLPHGQQRDQPQSVQTTAQSRPGDVCVPAPGRQSRPGTGLHHRVPLLPASPVRHAGRTHGGLLMGFFQTLLRGRTQP
QSVPADAPEDSGALDVAAAEAEATERYLARLAAMGIPLPNTGSKNGATQAEASRLYDHDPSFVDLLPWAIEYLPDEQVMLE
DGRSRAAFFELVPLGTEGRDPNWMQNARDALKEALQNSFDEHETSPWIVQFYAQDEISWDFQEQLRQYVHPRAGSAFS
EMYLALMKHHLEGISKPGGLFVDTAVSKLPWRGQQRVRMVVYRRIRKEDAQIRGQDPAAYLKSICERIQGGLANAGIVA
SRMGQGEIRNWLIRWFNPHDHLGQAEADLRRFYELVCRPDEPILQDELPLADGTFDSONLFYRQPVSDATQGVWLFDM
PHRVIVVDQLNKAPLTGHFTGETLKGDLNALFDRMPEDTLLCITMVVTPQDMLEGLHQQLSKKAVGDTQASIHTRDVA
TVRRLIGREHKLYRGAIALFVRGRDHTQLEERCITLSNVLLGAGLVPVEPQNEVGPLNSYLRLWLPNFDPNKRLEWYT
QMMFAQHIANLSPIWGRTTGTGHPGFTLFNRGGAPLTFDPFNKLDROMNAHGFI FGPTGSGKSASLTNLIQMLAMYLP
MFVAEAGNSFGLLADLAKRFGLSVHRVRLAPGSGVSLAPFADAIKLVESPDQVKVLDADIEASDSVQGSKADLEDDQRD
ILGEMEIVARLMTGGEKEDARLTRADRSVRQAILAAARTCAAANRTVLTQDVRDALYEASRSDTAPERRARIAEMA
EAMQMFCEMGADGEMFNREGTPWPEADLTVVDFATYAREGYAAQLGIAYISLLNTVNNIAERDQFKGRPIVKITDEGHIIT
KHPLLLPYAMKITKMRKLGAWFWLATQNIIDIPASGAPMLNMIWWCLNMPDPDEVEKISRFRLESPAQKSMML SARKE
SGKFTEGVLLAKGKEYLVRVPPSLYLALAMTENEKNQRYNIMQATGCDELEAALQVAADLDKARGLPFPPIVFPDQPA
VECQDE*

>ORF1040 (SEQ ID NO:15)

VPARRASDAPGGWAFARRILRTGALGHRGPRSQDLAERPGRISPALLRRARNLTLDPCVLRPGRDQLGQFPGAVEAV
RPSSSARIGLQRDVPGAHEASPGGHFEAGRTVRRHRRQQAALARTTAPRADGRLPPDPQGGCADSRTGPGGVPEIHLRAY
PRRPGERRRHRRFAHGRTGDQELVDPLVQAPGSPRPRGRGGPTSLLR TGMPSGRTDPAG*

>ORF1640c (SEQ ID NO:17)

VRLGLAEVIRVRVEPADQVPDILLSAHARSDDAGVRQAALDTLADGFQVRRRVLSANLRILLADPAVDHDPHAALLSSPG
QLADGGVDEQSARLRNALQVMLHERQVHLAEGRSSSRMDVLPQLLLEIVPADLVGLVELDNPG*

Fig. 4-1

>ORF2228c (SEQ ID NO:19)

GEPAQVAVQSRDFVLRFRHQAGAEQYVAQGDA AFLQLGMVAAAHEQSDRS AIELVLPADQASNGGHVLAGVD RGLGVTN
GLFRELLQMPFQHVLR RHHDGDAQQRVLGHSIEQGV EAI AFERLAGEVACQRRFVQLVDHNH SVRHGIEEPYALGGIGNR
LP IEQVLGEVSAVGQWQFILQDRFVRTAYQFVEAT*

>ORF2068c (SEQ ID NO:21)

SLCSRPIRRRTVATSSRVWIEAWVSPTAFFESCRCPPSSMSCGVT TMVMHSSVSSGIRSNRALRPSPLSVSPVKWPVSGA
LFNWSTTITRCGMASKSHTPWVASETGCR*

>ORF1997 (SEQ ID NO:23)

HPGLDPHPRGRGHRSTPDRPGAQALSRSDRSVRARPRYPVGGTLHHPEQRTARRRPGAGRTAERSRTAEQLPALAPLKL
RSKREASPGVVHPDDVRS AHRQPV AHLGAHHRYRTPWLHAVQPWRRAVDLRPVQQAGPADECPRHLRANWLRQVGVDPQ
PHLPDARHVPADVRRGSGQQLRPAGRLSQAVWPLGPPGAPRPGLRQP GAVRGRHQAGREPRPSEGAGRRRHRLGLGLP
GQQGRPRGRPARHPGRDGRPPHDYRWRREGRCAPDPCRSQRRPPGDPGGQDLRRREPHGTDPRRARCALRGLQER*

>ORF2558c (SEQ ID NO:25)

VGQQA EAVARFRDEHPRQVHGEHLADEVGQGRRLAGASWPED EAVGIHLPVQLVERVEGQRRATVEQREARVSGTGGAP
PDGRQVGDV LSEHHLGVPLQGSLLVWIEV*

>ORF2929c (SEQ ID NO:27)

SASRTSWVSTVRFAAAQVLA AARIAWRTALRSARVRRASSFSSPPVIMRRATISISPRMSRWSSSR SALLPWTESEASMS
SASSTFTWSGLSTSLMASANGARLTPEPGARRTRWTERPNRLAKSASRPKLLPASATNIRGRYMASIWQMRLVRDADLPE
PVGPKMKPWAFICRSSLNGSKVNGAPRLNSVKPGCPVPVVRPQMGDRLAMC*

>ORF3965c (SEQ ID NO:29)

APVGPYQAVDVVAAIHPRAALSAGRYPGDRLPSVESAAAPLSVQERISLASAGHPLRGSAGSGSGCRSGSGSANS ELSFV
LALHCRLVWENNGEGWQAARLVEIRCDLQGRLELVAAGGLHDVVALV LFFVFGHGQGVETRGNHTDEVFFALGQEHALG
ELAAFLAGREHHRLRRRQLAEPGYLLYFVGGHVQAQPLDHVQHRRPGGWDVVDVLGGEPEPGAQFP PHLGDLHGVGQQ
QRVLGDDVPLIGDLDDWPALELVAFGDVHVGVQQRDVGDPELGGVAFARVRCEIHHGKVGLRPGRAFAIEHLAVGAHA EH
LHGFRHFDPRAAFWRGAIAPGGLVERIAHVLGQYRAVRGGAGPGRRQDRLADGAAITGTQARI FLLFATGNHEAGDDLH
LAQDVSLVLEVG LAALDRVRLDVFVGVQHLHLVGALDQLDGVRRERRQADAGARGEAH PVDREAKPLG*

>ORF3218 (SEQ ID NO:31)

GAHHHQAPAAAALRHEDHQDVAETGRLVLARHPEHRRHPSLRGADAEHDRVVVVPEHAPRRSRREDIQVPRAVAGAEVDDA
LGPOGKRQVHRGRAPGQGQRIPRPCGSPESLPGP GHDRKRRKEPALQHHASHRLRRARGGLAGRSGSRQGARPATLPHCF
PRPTGSGVPGRMVLNSLTQNLIDNLTQILQNPEEDALQTLRICAPVLI EELQIQIQLRAVDRRDIVPQIKQLLDEWLQQH
PQPDTAQQALIEAVDRAEILQRRQA*

>ORF3568 (SEQ ID NO:33)

PKTKKRTSATTSCKPPAATSSRRPCRSQRISTRRAACHPSPLFSQTNRQWSARTNESSEFADPEPDRQPD PPAEPRRG
PADAKDMRSCDRGAAADSTEGSRSPGYRPADKAALG*

>ORF4506c (SEQ ID NO:35)

VNKFFVFRFTLQSSLVQFRKVQCAARQAPVAGRLSEDRIDSAPEGFGAALDPRALHQASLVAGRLAMHLQ GKMAPNQVH
VRMAVYPALKPRGVDLAEGALQVGVFIDRPARFRIAEAVVGWQALHQKLYPYGGCSQDDQQQPRPGQGGTLKSF GCPAA
LQESHACLRCRISARSTASMSACWAVSGGCCSSHSSKSCFICGTISRSTALS*

>ORF3973 (SEQ ID NO:37)

GRGPRGDPTAEASVRLKGGWAAKRFQGPALPWAGLLVLLAASAVGV ELLVKGLPANHSLYGDAKARWTINEYADLECP
FCKVYTPRLKRWVDSHPDVLNLRHLPLQMHGEAARHQARLVE CAGIQGGAKAFWSAIDAIFAQASNGGGGLPGGTLDFP
ELDQARLEKCAKDNEIDSDIKLDIDIARSKGITATPTLVIRDNQTGRSVKLEGMADETLLSAIDWLAKDL*

Fig. 4-2

>ORF4271 (SEQ ID NO:39)

TWFGAIFPCRCMARRPATRLAOWSARGSKAAPKPSGALSMRSSLSRPATGAGCLAAHWTFLNWTRLDWRNVRKTTNLLTQ
ISSWTSTLHGRRALQRPSPSSSGTTRDEA*

>ORF4698 (SEQ ID NO:41)

EIGEDSNIPLLVLQDALHFTWQNLDLLPIHNLVHSLVAGAGEAKPQLHCRPSIDVNALEQALHDFDHSLSISVSQSLHTGIM
LPRTCRRHPYLCTWQRSITARKNTPPTS*

>ORF5028 (SEQ ID NO:43)

FPAALSEVILSAVCTFLEPVQTHASSSLPPWPAATNAGRWRRTGTAEQRESGRNLGHRQGSGLCHRIVARSVSGRPGT
PRGATDCGLAPGSTACSSGV*

>ORF5080 (SEQ ID NO:45)

NRYRPMPLHHSPPGRRPPTLAVGVLLVLLSSASQAETWVITDKAHPVSATGSSRVLFDAQEHLEEQTLAALPQDPQHAQ
AAFKRLQSPDGRRLLQAEKVKAQQDVADAWSLGVEKIPAVVVDQYVVYGEQDVSRALIELIAKARRSR*

>ORF6479c (SEQ ID NO:47)

FVSVSLLEVGTADHPLALAAAGVGTPERPGVLPVDGLRLRPRVGKHAVERAQQWGQQLPFPGRGIALFQLARRPVAVLG
GCAHGEVDVELADSRGDIAGALGDDGCRLLVVGLVQEAARIEVPPHVAGEDSTHLAQPWDQRFVHLLGNSMPPANGVQ
CAEKVRHQDGGARANVPRGAGEPAERGATRMADHIFLEAADAVLGLVVCGRVIAGLGWIRCTQRRYLGPVAPGIRV
AGDDCVRHVVADLDRRLHFAAMRAAEQPVTDPDLLVFEALRGKGGGDDGSAVDRGRGREREAEQGGRRCCAAEVEAGHQ
DLLALAISSRARETSOSP*

>ORF5496 (SEQ ID NO:49)

ANRQGGQVALMTSLNLRRLAAAAATFSLSFTASAAINSAAIVSSTLSPQCLEYKVVGICYWLLCGPHGCKVKTSVKVRHY
VPDAVVSSYANTGSPNPTVEVSALGTPNPLAQAGNDATTNYKAENSIGRFKEADVIGHPPGATFSRFASASGYVCPGATVP
LVPYFLSTLDAIGWRHGIPEQVYPEALVPGLEVGIGFSGDMWGNLYPRSGFLHQTDYKTAAVIAQAGDITTRIGQLH
VYLPMAAPKDGYPAGELKEGDASTGKWQELTPSLSLNCAVFPNSGPKTQAVDGEHAWALWRPYSCCQRKGQMFICSTD
FQ*

>ORF5840 (SEQ ID NO:51)

RDHKLQGREQHRPLQSGGCDRPSWWRHVQPVQRQLWVRLPWRHRPAGAVLSQHTGRHWLAAWNRSAGVPRSVGPRAARGG
WNLLRRHVGEPLSAQRLPAPDRRLQDGSRRHPARRRYHHANRPAPRLPPHARSPOGRLLAGGRAERGRCLDREMAGADPI
PEPQLRGVSQWLWEDASRRRGARLGALASLLLLPAQADVHLQYRLPIRTRRRIMRMNITSVALMWLLAAQLAQADDPIN
VSKTGTVLSDVLYSIGGSAVSMGSAGQMSIGVGFGWNNMMCGNMNLSTTLENQLNGATQGFQNIIMGSVIONATGAV
MSLPALIIQRANPOLYNLITNGILQARIDYDRSGTKCTIAEKMADIAGEQTGWGKIAEQALGATLASDGKDAVSALEA
VEKKGGNDGVTWGGDKAGSGQKPIRIVNDVTRAGYNLLTSRVNDSSSVPSATCNGLVCNTWSSPQEAFAFATRVLG
EQQQOTCEGCQKTVTAAGVGLTPLIQETYDKKLSLQELLSKSKPLTAENLAAAGTDALPITRGVIEALRDERDQDVLAR
RLASDVSLMDVLSKALLQRLMFAGAKEPNVAANGLATQAVDQOTSLQOEISNLKTELELRRELASNSPMRVIERGQQR
ASGSSGVFESAPDADRLDRLQAPSAAAGKSGGRP*

>ORF5899 (SEQ ID NO:53)

SAILVAPRSAGSPAPLGTALAPPSRWCRFTSAHWTPLAGGMEFSPRCTPKRWSQGCARWVESSPATCGGTSIRAAASCT
RPTTTRRQPPSSPSAPAIAPRESASSTSTSPCAQPPRTATGRRAS*

>ORF6325 (SEQ ID NO:55)

ASTARCFPTLGRRRKPSTGSTPGRSGVPTPAASARGRCSSAVPTSNDTETNHANEHHLGRANVAARSATCPGRRPDQRV
QDRHGAQRRGPLQHWRRQCGEHGQRRPDGLDRRLRLQQRHDVRKHEPEHHPGEPAQRCHTGFPHEHGLSHPERDRRGHV
AAGVDHPAREPSALQPDHQWHPAGADRLRPLERDLQNDRRKDG*

Fig. 4-3

>ORF7567c (SEQ ID NO:57)

QCLAEHVHQDGRQARQDVLVTLVAQRLDDAAGNWQSIGAGRSQVLCQWQFALRQQLLQRLLELLVVGLLDQGEADAS
SRHRLAFAAGLLLLPQYPGGECGGLGGGSPVADQAVVASGGRHARRI IHRAAGQQVVARPGHVDDANGLLAGAAGL
VSTNPGYAIVAFLHCFEGGYGVFPVRGQCGAQLAFGDFPPAGLLASDVSHLFGDRFASPFRAVVDPRLQDAIGDQV
VELRVRALDDQRRQRHADRAGRVLDD*

>ORF7180 (SEQ ID NO:59)

FVERAFRHLQQRPGLOHLVLPPEGRRIRHPGTGGATATDLRRLPEDGDCWRRRPHPADPGDLRQEAPVAAGAAVEEQTTD
CREPGCGRHRCSSANYPRRHRGAARRA*

>ORF7501 (SEQ ID NO:61)

PGRPAGPPGVRCPLDGRAQQGTATAAPDVRRRQGAQRRRQRPQHPSRRSADQPPAAGDLQSQDRTGTPSRVGGQLPHAGH
RARATTRLRVQWRVRVGARCRSPSPAGPLCRRRQVGRETMADTLTRKLLGQLLVGLVIGLAVVGTLLSLFALNH
GGIQGLEAWRQSNYWSLFAWRALLYCALAIWFRQKELSAHERQIRRIEILVLLLVLIEFSKAYFRTGGAA*

>ORF7584 (SEQ ID NO:63)

CSPAPRSPTSPPTAWPPKPSISRASCRRSPISRPNWNSVASWPATPPCGSSSAGNNAPQGPVACSSRRPMPIASIACR
PPLPPAASREGDRDGRYAHHPKASRSATGRSADRHTGSGRYAAQSLRPEPLRWHPGPGGLAAKQLLELVLRLAGAAVLRP
GHRLVPAAQGTERA*

>ORF8208c (SEQ ID NO:65)

RSCCASRAEVGFAEFDEQDQQQHQLDPPNALPLMRAQFLALPEPGDGQGAQVQQRPPGEQAPVVALPPGLQALDATEVVQ
GEETEQRTHCQSDDDQHSQ*

>ORF8109 (SEQ ID NO:67)

AAHSADRDPGAVAGPAHRIQQSLLPHGRRSMTFMTNDYLEYYLTLLGWIINNGIWNMISDTGLFAVPFAAIVMREWLV
RGEADEGNKGVLSLARIETHIYGVYIVVALAGIPVNVSFDTIEFDQTRAQQCQYNLPAPADTGWSSSFSSLAGKSAQM
PLWWAMMHLSKGTSGAIAAIPCGTDLRQMRMEVDNTRVNNPLLAQEIADFSDCYGPSRARLFMRQPDLSVAEDNKA
LQDLNWIGSRFLNTPGYDDTDYSKSPRQSWPYNATRDAGLPQVGGGGGYPTCKQWADSGIGLRDRIKDQVDPDLMTSF
LKWAKWLNQDEVTEAVIRQVISPSQVKGNYTYDGGQVGGTVWNGIARTAGTFGVAVGSLAYFPAMDVMVRQALPMVMSF
LKMAMVICIPMVLVIGTYQLKVAMTMTVVFAMMFVDFWFQLARYIDSTILDAFYGSQSPHLSFNPVMGLNTATQDAILN
FVMGSMFIVLPLWMTAIGWSGIQAGSVLNLRSRGTEGVQAGKEAGNRVKNVAV*

>ORF9005c (SEQ ID NO:69)

VSPPLLAGVWAATTAHLRQAGIAGGVVGPRLTGTLRVVGVVVRGVQQESGADPVQVLQRLVVLGDGAQVGLPHEQPRTG
RPVAVSGKISDFLCQQRIVHARVVHFSHLPQIRAAENGRDGAAGEALCQGVHHRPPERHLRTLQAAEGARPAGVRR
RQIVLALLGASLVELDGVEAHVDDRPQGDHVDVDMRLDAGERQHSLSLVALVGAFFTNFQPFQAHHDGREHREQASIR
DHVPDPVDDPAEEGEVILQVVGHEGHAAPPVRK*

>ORF8222 (SEQ ID NO:71)

LPGVLPHPRLDHQQRDLEHDLGYWVVRGAVRGHRDARMAESSWGRRRRGQGSASVSRPHRDAYLRLHRGRPGGDPGRQ
RELRRHVRPDSRPVPIQSAGTGGHRLVELLQPGRQECADAALVGDDARPVQGLHQRRHRHGSVRHGSAADANGSGQH
AREQSAAGTRNR*

>ORF8755c (SEQ ID NO:73)

QSLEKSAISCASSGLFTRVLSTSIIRICRRSVPHGMAAMAPLVKPLDRACIIAHQSGICALLPARLLKELDQPVSAAGRL
YWHCWARVWSNSMVSKLTTLTGIPARATTM*

>ORF9431c (SEQ ID NO:75)

LKPEVDEHHRKEDDRHRHGNFQLIGADDQDHRNADDHCHLQERHHRQCLADHIHRRREVCQAAHRNAEGSCGSRDAVPHG
AAHLPAVIGVDVTLDLAGG*

Fig. 4-4

>ORF9158 (SEQ ID NO:77)

RLHRLRRAGGRHRVERHRENRRNLRRCGGQLGILPGDGYGPPGTADGDVVPEDGNHGLHSDGPGHRHLSTESCHDDDGRL
LCDDVRLLVSVSQIYRQHDT*

>ORF10125c (SEQ ID NO:79)

VIAGCLPLGARRLMMNAHTNKGFASTRIGFGLGMLVRFCLHRRPALRWVKRVSFLLLVALVVSQNFMWLAGVSMITLLCVF
LVGFALVKGDISVSKGSPSRDVSTMTSQAETESVAELFDYQAAHHYRD*

>ORF9770 (SEQ ID NO:81)

SNSSATDSVSACEVIVETSRLGDPLETEMSPLTKANPTRKTHSRVIDTPASHIKFCDTTRATNKNRLTRLTQRRAGRRSC
RQKRTSIPRPKPIREAKPLLVCIFIINLLAPKGRHPAITYTPKKMIWQALWHIMPLAICRLEYLMATRNVLDPLEQDI
NELVETGRYQNRSEVIRAGLRLLLOQEAQIAKLETLRNATSSGLMQLERGEYDEITSDELAQYLDLGNQASH*

>ORF9991 (SEQ ID NO:83)

SWTAIMQAEETHKHTQTKTDPGGKAFVGVVRVHHQSPGSQREASCYHLYAEKDDLASIMAYYATSYLPTGVPHGNARRPSR
SAGAGYQRRAGDRPLSESQRSHPGRLAPAAATGSPDRQARNPPQRNQWADATGARRVRRDHQRRTPIPRRARQPGEPL
KHGQVPHLS*

>ORF10765c (SEQ ID NO:85)

HLVCRHPVEDEVPGPNLTDIGHRVAVNEVDAAQASSQFFTADAAYLLWVCNCFQRRPYECLVTSARGIAEVVVGEAQD
IDDVRLGIMRDAVLGHASVARLVAELVEVLGQFVAGDLVLAALQLHQPTGCCVAEGFELGYLGFLLOQQAQACPDFAA
ILIAAGLHQLVDILLQRIGKDDVSRCHEVLQSADS*

>ORF10475 (SEQ ID NO:87)

SMAKYRISHDAQADIVDILRFTHNHFGDAARRRYQALIGAALAEVATDPQQVGSISREELGAGLRSIHLVYCHSMPNVGK
VVRPRHFVIFYRVATDQVLEVVRVLHDAMDVDQHLPR*

>ORF11095c (SEQ ID NO:89)

SRMQAVVSTNANAWSGGMQSSGQATAIAHQPWGTCWWMFTRSLFVFAGANAALSAFRQALSGRAFTLVNHSILRPSSPFPL
WAICSCYSCSSLGQVLIHIGVVKHANHL*

>ORF11264 (SEQ ID NO:91)

TAVRRDLLKLMGCTHIEADYIGGLRCSTAPEGTWVAHGFGPIVDVIDDSAGFFSTHRLALHYPAQCGLAVDQAIPTAI
HVASPLMHVCIGKVVISAWMC*

Fig. 4-5

>ORF11738 (SEQ ID NO:93)

EEVIMKLQAYRLQNYRRLRDVVIELDDDEISIFVGANNNGKTSVAVQGLYSMLRGEVKKFELDFSAALWAEIDAVGRTPPG
DEDAPKRLPSILLDLWFRVGEDDLATAMSLLPSTEWGKCVGIRVAFEPDAHELWKFHELHEKANNAVALAAKRKAA
GEQAVEAGAEDAAAVVADAGEYKPWPESLTKYLTKELSKEYTFRYVYVLDERAFVGYQAREADYEPLPLGKEPGGAAILKS
LVRVDFLRAQRHLDDPDAGSSDRAESLSRRLSRFYHRNLEKRGDDHAALKALDTSEKELNFHLKEVFNDTLTRLAKLGY
GVNNPEIVIRAALDPTTVLGQDAKVHYVIPGVASAQLPDSYNGLGFKNLVYMVVELLDLHEQWKAEDDKRAPLHLVFIGE
PEAHLHAQIQQVFIRNVRLLEDANDHATLFHTQLVITTHSPHILYERGFSPIRYFRRVNDQLGHHTDVRNLSLFTGAS
DAPAREFLQRYLKLTHCDLFFSDAVILVEGNVERLLLPAMIELVAKRLRSSALTILEVGGAFARHFQELIAFVGLTTLVI
TDLDSVTVKTDAAKAAQGAAGAEGAVDGDDEDEDDDLKPFLEDDDEAEPSGKKKSKRGSTCHAHVEGAVTSNQTLISW
IPKKRSMABLWEVTAEQKTLSLAEDSSAGVRVAYQTKVSVTVGATTSQLCGRTLEEAFGLENADWCQAEANRSVGLKLR
APSSPEELAELHDRVVGKNFDKTRFALEVLASGPLNGWKVPAYIAEGLAWLEAKVAHELEADAAIATEVATIEPTTADV
VAIIVDPGQTA*

>ORF12348c (SEQ ID NO:95)

RKVYSLSSFFVRYFVRLSGQGLYSPASATTAAASSAPASTACSPAALRLAASATAALLAFSCSSWNFQTSSWASRGSNAT
RIPTHLPSSHVLGSSDIAVARSSSPTRNQRSKSMDGNLLGASSSPGGVLPTASISAHSAALKSKSSNFFTSRPSIEYRPW
TADVFPLLLAPTKIEISSSSSMTTSRSR*

>ORF12314c (SEQ ID NO:97)

GTSSGFLAKACTRRHRPPPPQRLPRPPQLAPRRPCAWPQARQLRCWPSHVHGTSSRRARGHPEARTLPGSRRTCRTQC
SAAATSQWRGLHRRGTRDPRVWTVTFWAHPHRQGASCRPHRSRPTAPH*

>ORF13156c (SEQ ID NO:99)

RQIAHIRVMAQLVVDAAEVPNGRESAFIEDVRGVRGDDELVEQSRVIVSILKEAQNPDEDLDLRVQMRLRLNEDQM
KRSSLVILGFPLLVQVEQLNHHVDQILEPQAIIVAVWLGGSYARDHVNLGVLPQDSGRIQGRPNHDLRIVDARIAELGQ
AREGVIEDFLQVEVQQLLRGI*

>ORF12795 (SEQ ID NO:101)

LPPNCQTATMAWGSRIWSTWWLSCSTCTSSGKPRMTSELRFIWSSLSRLRRICTRSSSRSSSGTFCASLRMLTITRLCST
RSSSSPRTPTSSMNADSRPFGTSAASTTWAITRMCAICRYSKRARPTLQRANSCSGI*

>ORF13755c (SEQ ID NO:211)

ATRTPALESSASDSVFCASVTSQSSAIDRFFGIQLMRVWLDVTAPSTCAWQVLPRLDFFLPLGSASSSSSSSKGFRSSS
SSSSSPSTAPSAPAPCAAFAASVLTVTLSRVMTSVVSPTKAISSWNRCANAPPTSRMVRAEERRRLATNSIIAGRSRR
STLPSTNITASEKKRSQCVSFRYRCRNSRAGASDAPVLNSDRLRTSV*

>ORF13795c (SEQ ID NO:213)

CRRTHRHRNLGLVSYNPNSAGILSQRQRLLLRRDFPELCHRPLLRDPADEGLVGRDGTFFHVCMAAATLLGLLLATRFCE
VVVFKEGLEQVVVLVLVISVNGALSACALRGGLGVRLDRHAVQIRDDQCEPNEGQDQLEPMRETTDFKDG*

>ORF14727c (SEQ ID NO:215)

QEVGELKDVLAKEYALGVVTAHAVVERPDAGHSLQASDISLLVGLVPVARGLPDTRAVILELFFKFGDPPADVVLQPNLD
VGLERLCNRPVKAVDGRDMNQRVIVDVRQDFIGKVGIRDARDYLLPRPHAGAVLRDHPVQRLDEGGGLAGTCASTNHEG
LRRRRYNACVDLAVGVGIWAINSSAHAVCPGSTMIATTSVVGSIIVATSVMAASASSSWATLASSQAKPSAMYAGTFQP
LSGPLASTSSAKRVLKFLPTTLCNFSASSSGLLGARLSLRPTDRFASAWHQSAFSRPKASSSVRPQSCDVVAPTVTET
LVW*

>ORF13779 (SEQ ID NO:217)

RWVRRHHSSAAHLRRPLVLRTRTGARLQTRGRSASSSSAHRAALKSWLRSYTIIGWSARTSTRPALRWRYSQAGRSMAGR
FPRTSPRAWPGSKPKWPTSLRRMLPSPPRSRLSLRLQPMLSLSLLTRGRRHEQTN*

Fig. 4-6

>ORF14293c (SEQ ID NO:219)

GRWSCRNLQHEPRRAAEASLQCMRGSRRRRYLGYQFVCSCLPRVNNDSNIGCSRLNSRDLGGDGSIRLKLVGHFGE
EPGQALGDVRGNLPAIERPACEYLQRKAGLVEVLADHPV*

>ORF14155 (SEQ ID NO:221)

PGADGMSRRIDSPDTADREIHACIVATPPQPFVVRAGAGSGKTTSLIKALDWVISEHGASMRARKQIVACITYTDLATN
EILADVNDPLVHVSTIHSFYWSIAKTFQADIKVWLQNDIRRRRISELEEFENYSSRVQTTDRNKADQERYVRSLEAV
AGVRTFNYGVGSDYAKGILGHEDILQLADFLQNRPLFRRVVALSYPPVFIDESQDTFPGVVKSFKEVEAQMKGKFLGF
FGDPMQSIIFMRGAGDIQLEDHWRAITKPENFRCAKQILDVANAVRAQGDGMEQVRGLHERVDGNLKLVEGSARMFVLPNT
LNRTEALARVRAWSSATNNDEGWTPDIAVKILVIVHRMAANRLGFGGIYSALNDKTSAMKQGMQDGTGWPVRPFLSFA
LPIVA AVKAGNEFAAMSLREFSPRLAPAALTGRRADVRLRELHAAASRLVAMLDEAGTTIGDIALHLCDTGLFEFDERY
ARVLGFVRDIADTAQPEAADAVPAEGLSLDATMAKFFNCSAQELWPYERYVSEGSPYATQHGVKGAQFERVMVMDDEE
SDYRTYNYERVFASAEARAADRARALDGDENTWSRTLRLLYVCCTRAQRGLVLAFFVADPATTLENVVASGILPRSAVFT
QEVLVGWP*

>ORF14360 (SEQ ID NO:223)

SRASRIPTLPPMKSWRTSTMTRWFMSRPSTAFTGLLQRRSRPTSRFGCRTTSAGGSPNLKSSRITARVSGRPRATGTRP
TKSDMSEAWRLWPASGRSTTAWAVTTPRAYLATRTSFSSPTSCYKTARCSGDSWR*

>ORF15342c (SEQ ID NO:225)

EGSNGPTGAVLHPLHGIIRRLVVQRRVDAAEAKPVCGHAVHDDKNLDCDVWGCPTLVVVRRAAPRSDSCQSLGSVQVRVQ
DEHPGRPLHQLEVPIDPLVQPADLLHAIALRAHGIGVDKLLGAAKVLRRLRDGPPMILKLDVPCASHEDRLHRVAEKTKA
ELALHLGFHFLERLHYTRERVLTLIDKHERVAQRHDPSEQRAVL*

>ORF15260c (SEQ ID NO:227)

MPPKPSRFAAMRCTMTRILTAMSGVVQPSSLFVAELHARTLAKASVRFSVFGKTNIRADPSTSLRFPSTLSCSPRTCSMP
SPCARTALATSRICLAQRKFSGFVMARQ*

>ORF14991 (SEQ ID NO:229)

RRQCRARAGRWHGASPRAAAREGRWEPQAGGGVGPDVRLAEHAEPNRGFGKSPVELGDEQRRGLDNPRHRSQDSCHRA
PHGRKPAWLRRHLLGAERQDVGCHEARDAGRHLARSTLPKFCATDRCSCEGRQ*

>ORF15590c (SEQ ID NO:231)

RSSNSKRPVSQRWRAMSPMVVPASSMATSLDAAACSSRNTSAARRPVRAAGARRGLNSRSLIAANSLPAFTAATIGSA
KLKRGRTGQVPVPCIPCFMASDVLFSFAE*

>ORF15675c (SEQ ID NO:233)

SFGRNCISSLGLLSGVSNIPDKPKNTRIALVELKKTRVTEMESYVTNGGPCLVQHGDKPRRSSVQLSQYIRGTSAGQSRR
RQARAEFFPEQAHRRRELIAGLHSCNDR*

>ORF16405 (SEQ ID NO:235)

IDLKRCVGSLEKCCFACKETIIHVHAIRCRQCGESQGWRRFMSSPTSVVALVLSLLSIAATKPERLFDAQRAELQISIT
GGDYKAAQLMLTNNGSKPATLVSFETSKATTNTKTWFLVSNTDGEILEPGKTYKIRASTDESIPKIVEAERTILKSQY
ALADNCELTAKEYEATGQKVVRVQPFMCDTPPEKGGLPPGKPGIPIWYLGQE*

Fig. 4-7

>ORF16925 (SEQ ID NO:237)

RPRGRRLCVCNRSCATHLLKRVACPLVNLAYPFGTLVKNDVFMPPWALTPIKQSCVRSSNTSLAQLNDCYVYGCCRYVIP
WPYAYEVNSESQWTIFLLGVDCSGKVIYFRNTARVGPFLAASIYRPWYGSDALVLHFTK*

>ORF17793c (SEQ ID NO:239)

AKMIVIDKNLEHLVAQCAICEKTLFDEFSLKIQLGHTYYEPKSLPASASIVYGSHAPSTFFLEPKEIQQNLVLKSGEQV
ITCSKHRYKIPLDYFGLVQTKGTLARLFVQVTCNDGQVEPGFDGYVTLIVNMSPWTIEIPAVSDIAQLYLKCSASE
PYHGRYMDAAKKGPTLAVFRK*

>ORF18548c (SEQ ID NO:241)

RTMAGWPRLAAQGRRTNLMSVLQIKGRITTKSHTDFDAASYSSNSLILTDAGDERIEEFSLELSVGEWSDNYSGNDKNLW
RIVDGMTIRGHDSVVVEAAEEIKVPHNRYGIVLPTGSLFLSRGVLVASAKVEPAFDGKLLRIFNTTNKNVCLTKGEKLG
SVIFFSTESTHTQSPIKRGSEISTLPITRRARLKKWFSLNPTIIVGWTLNLIGSSLVSSIMYAVYYKVVLEHQSQPPQS
QQNAQPSPEVKPK*

>ORF17875 (SEQ ID NO:243)

TAYIREDTRELPIKFSVHPTMVGLSENHFFNRARRVMGSVDISLPRMLGLWVCVDSVEKKITEPSFSPLVRQTFLLVV
LNILSLSLPSNAGSTFAEATSTPREKRPLVGRTPYRLCGTLISSAASTTTES*

Fig. 4-8

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>ORF18479 (SEQ ID NO:245)

SVTHSSDLSFVLGLRDAATLPLSFIPADIPGYRLKDDVRKACTNLNFKRLAVIVGERERHRPYITWRQHTGTERYPASEQ
RASRKKKRRQIFRQIEFFHGARQISLARFHDCAVIRVCEHDLARGASRRFSQASTPYCQAREACESEVKSNAFRGGQLT
VGKVL*

>ORF19027c (SEQ ID NO:247)

MIYSPHSLKLVRDGKLIKHLAHLRELTTPGEGVDFLRLAGLSRLTVGGSLRESTRRTTPASEVVLADPDDCFVMEPGKTY
LASTMEFDLPEDLAALFFPRSTLFRSGITFSSSVLPPGYVGPMTFALTNNHSEAFEIQIGARFAHVIFQAVSGDIGRYK
GQWQGRVSQPKDEGQI*

>ORF19305 (SEQ ID NO:249)

WPFSACRLFGMTGQVGCKRWSAPMQLGGHVRCNYAVEPGVPVPPKQSIRPRWHIANKIPFPATVVLSELLPALIWRKSPLHE
SSWSLPCFNSFFPGYPSRPPQPKLPQGDSSFL*

>ORF19519 (SEQ ID NO:251)

SGGKARSMNRHGASHVSTPFLDIQEAVPHPNQSCPRGIHPSSEQHGHTARHASPPAATGEHLAARLAIQAAIRGDLPAAT
GQLCRAGPAAPCFGKSSPCPSRRDDRSRPGDRGLRTQGTADLPAPDRRSAGVTVSPG*

Fig. 4-9

Fig. 4-9

>ORF19544 (SEQ ID NO:253)

IVMEPPMFQLLSWISRKPSPTPTTKAAPGGFILPLSSMELLGTPRRRQLLENIWQRASLSKQQFEEIYRRPLANYAELVQ
QLPASENHHHAHPGGMIDHGLEIVAYALKVRQTYLLPIGAAPESQSAQAEAWSAAAAYGALAHDIGKIVVDLQVELQDGS
TWHPWNGPINQPYRFKYVKSREYQLHGAASALLIHQLLPRTALDWLSRFPPELWALYLYLFAGQYEHAGILGEIIVKADQA
SVAQELGCGNPDRAAPKQSLQRQLADGLRFLVKDKFKLNQPSGSPDGWLTQDALWLVSKEADQLRAYLLAQGIDGVPS
SNAPFFSMLQDQAVIQTNAEDKAIWTATVDNGAGWRNKFTLLKIAPALIWTDAERPSPYSGSLVVEDGTASTEKPETTC
EIPNGPAEQQQAPETKMMLHQPAPSVAKPANETQAIAPSTDDQEETDDLYALLGNINSPLEELDTSHDSPAASPTNTRG
EENLQQLPGTKPTDCAPEAIEDVFMPSTDLGQGFVGMWKSIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQE
HPVLEKLAQAKETTGWKLVRQAFKQGLHRKTSKNLNIWTIKVSGPRKTKELKAYLLQDPKLLFPPEQPLDNPSLTVITDA
EGGVE*

>ORF20008 (SEQ ID NO:255)

ATGRQHLAPLERTDQPAIPLQVREVPRIAPRRCLSTSHPTATAHCTRLAQSLSRVGSIDLPRVWAVRARRDPRRDHR
EGRPGLSCTGARRQSGSSSGCTEAVAAAAGRRPSLLGEGQVQVEST*

>ORF20623c (SEQ ID NO:257)

RELVSFSSSTVVYGRPNGLVLGICLDDGLVLEHAEERRVRGGHPIDTLGQQVGSQSLIGSRLAHQPECVLGQPSIRRAARL
IQLELVLHQEAKAVCQLPLQLRLRCSQSSIRIAS*

>ORF21210c (SEQ ID NO:259)

RLKIPGVTSMAVPSTVCTKALVSLMNRRAAMPDFIQPTNPCPRSVLLGINTSSIASGAQSVGSLVPSGCCRFSSPRVF
VGEAAGESWLVSSSSSGELILPRSAKSSVSS*

>ORF21493c (SEQ ID NO:261)

AAAASFHTSFGIGDDREAWVVQRLRLREQQFGILEQVGLFRLARTRNLDGPDVQVFTGLPMKPLFFERALHQLPAGRLL
GLGQFFKHRMLLDIALENSWRDQHGGPVYGMHQSGLGVVDEQATGRDARFHTNESLSQIST SARHKYIFNCFRSAICWLL
GP*

>ORF21333 (SEQ ID NO:263)

TSGPSRFLVLARRKSSRPTCSRIPNCCSLSSLWTTQASRSSMPKEVWNDAAAHRGVHLRARSPPGSQREDLPRRDQGA
QALRSYGNRTGRGPPGCPGMATQGTGTRPVQAELEHVLESSADDLGLCHRA*

>ORF22074c (SEQ ID NO:265)

VRHKPLRYWHYELFVSLCLAADEDQLIFPVDVALADAQQRIQPDAGEVEDLKRAKPEPGGRDPCAFAGAALCAVLHVEP
IAGEQDGFGGDGFACSPGGNDGGLSERVDLGVRHQLMLDGIAPDRPQMI RVRVPAPLGQALFQYLASPSQDSFVVHVLYG
CRRTEVLEQLRGRGAVDLRAGFPEIVREDVLLGELLRRHSTPPSASVMTVRLGLSRGCSGNSNLGWSR*

>ORF21421 (SEQ ID NO:267)

AASGQPKPHGHRCRRRCGMPQQLTEEYIFAHDLREASAKIYRAATKALLKHFGPTATVQDQVDHRAVLGWRKRVLEQGL
SKRSWNTYSNHLRTIWGYAIEHELVTHSQVNPFRKTTVIPPRASKTVAAEAILLARNWLNMQDGAERCTGERARITPAW
FWLCTFEVYFTGIRLNALLCIRKRDIDWENQLILIRGETEKTHKEFVVPITEGLVPHLSRLLQEADRAGFADDDQLFNV
NRFSPHYKSKVMNSDQVEAMRKLTKEKVGVRMTPHRFRHTLATDLMKAPERNIHLTKCLLNHSNIQTMSYIEADYDHMR
AVLHARSLAQGALENVRKVDYSGSPQASAKPKCGQPLARVSEAPPPEARTEPAEPREHTPGTGIQGGPTAWEADALPQP
PDTFEPVSLFTLMAQNLSNRAASASAAPAATSGSGGWGSAARSNLA*

Fig. 4-10

>ORF20008 (SEQ ID NO:255)

ATGRQHLAPLERTDQPAIPLQVREVPRIAPRRCLSTSHPTATAHCTRLAQSLSRVGSIDLPRWAVRARRDPRRDHR
EGRPGLSCTGARRQSGSSSGCTEAVAAAAGRRPSLLGEGQVQVEST*

>ORF20623c (SEQ ID NO:257)

RELVSPTSSTVVYRGRPNGLVLGICLDDGLVLEHAEERRVRGGHPIDTLGQQVGSQSIGSRLAHQPECVLGQPSIRRAARL
IQLELVLHQEAKAVCQLPLQRLRLCSQSSIRIAS*

>ORF21210c (SEQ ID NO:259)

RLKIPGVTSMAMPSTVCTKALVSLMNRRAAMPDFIQPTNPCPRSVLLLGINTSSIASGAQSVGSLVPSGCCRFSSPRVF
VGEAAGESWLVSSSSGELILPRSAKYKSSVSS*

>ORF21493c (SEQ ID NO:261)

AAAASFHTSFGIGDDREAWVVQRLRLREQQFGILEQVGLFRLARTRNLDGPDVQVFTGLPMKPLFFERALHQLPAGRLL
GLGQFFKHRMLLDIALENSWRDQHGGPVYGMHQSIGVVDEQATGRDARFHTNESLSQISTSAHKYIFNCFRSAICWLL
GP*

>ORF21333 (SEQ ID NO:263)

TSGPSRFLVLARRKSSRPTCSRIPNCCSLSSLWTTQASRSSMPKEVWNDAAAHRGVHLRARSFGSQREDLPRRDQGA
QALRSYGNRTGRGPPGCPGMATQGTGTRPVQAELEHVLESSADDLGLCHRA*

>ORF22074c (SEQ ID NO:265)

VRHKPLRYWHYELFVSLCLADEDQLIFPVDVALADAQQRIQPDAGEVEDLKRAKPEPGGRDPCAFAGAALCAVLHVEP
IAGEQDGFGGDGFACSPGGNDGGLSERVDLGVRHQLMLDGIAPDRPQMIRVRVPAPLGQALFQYLASPSQDSPVVHVLYG
CRRTEVLEQRLGRGAVDLRAGFPEIVREDVLLGELLRRHSTPPSASVMTVRLGLSRGCSGNSNLGSWSR*

>ORF21421 (SEQ ID NO:267)

AASGQPKPHGHRRCRRRCGMTPOQLTEEYIFAHDLREASAKIYRAATKALLKHFGPTATVQVDHRAVLGWRKVLQGL
SKRSWNTYSNHLRTIWGYAIEHELVTHSQVNPFRKTTVIPRRASKTVAAEAILARNWLNMQDAERCTGERARITPAW
FWLCTFEVFTGIRLNALLCIRKRDIDWENQLILIRGETEKTHKEFVVPITEGLVPHLSRLQEQADRAGFADDDQLFNV
NRFSPHYKSKVMNSDQVEAMYRKLTEKVGVRMTPHRFRHTLATDLMKAPERNIHLTKCLLNHSNIQTMSYIEADYDHR
AVLHARSLAQGALENVRKVDYSGSPQASAKPKCGQPLARVSEAPPEARTEPAEPREHTPGTGIQGGPTAWEADALPQ
PDTFEPVLFITLMAQNLSNRAASASAAPAATSGSGGWGSAARSNLA*

>ORF22608c (SEQ ID NO:269)

RICFPRGWSLNACPWRVLPWFRCRLCPGLRWRRFTHSSERLPAWLRFGRGLRGAAVIHLDPILQALGQASSMQHGTHVI
VVGLDVAHRGLDIRVVEQALREVNPLGCLHQVGGQGVPETVRGHPHPNLLGQLPVHGFDLVGVHHLALVVR*

>ORF22626 (SEQ ID NO:271)

HLRTKRAVHSDGSKLIEPCRLGIRGSRCKRIRRMGICRPKQSR LAIPVLRAGYRTKGSRAQQIVRPVGKIWNRYRERLD
SSAGMLAEPAQFQGYHSTLCNR*

Fig. 4-11

>ORF23228 (SEQ ID NO:273)

RDSNSRHPAPKAGALPDCAIPRLEFGSATWTRTRDPMINSHLLYRLSYRGTSFFQPWTLPVLLDSRLRGAPFYGCARACQ
 PSDPKSFSSFTSDKTALPLHAAALSRLPDAHEKAPPKRGFPCCPPKRSGEDDLVAFHLRRDTGTRREFAGDQLRQRVL
 DPALDGPLQRCACIDRVEADGNQLVQRLLAQFQAQLALGQALAQATELDLGDAGDLLASQRL EHHHFVDPVDEFRTFVRI
 DRVHHCGLRLAVAGQLDLRRTEVGGHHHGVAEVHRTPTVTVGQASVLEHLEENVEYIRMGLLHLVQQHHRVGLAADRL
 GQVAAFLEADVARRRADQAGHRVFLHELGHYIHPQRLLGIEEELGQRLAQLGLAHPGRAEEEEERARPVRIGEAGARTAH
 GVGHGDYRLVLADHSPMQLLLHAQQLLALALEHLRHRDTGPLGNHGFDFLVGHLVAQQVLGLAVLVDHLQAAAFQVRDGL
 VLDARHALEVALAPRRLHLLGLLDLLDLRRLHLGLLGLPDLLLEVGVFALEDDILLQLGQALPGGFVFLQLRLALD
 LQLDQATVETIQFLRLGVDLHADAAGGLVDQVDGLVRQLPIGDVAVRQLGRGDDRAVGDAHPVVHFI AFLEATEDGDGVF
 LARFVHQHLEAALQRGILLDLAILVEGSSTDAVQLAARQSRLEHVAGVHGTFRLAGADHGVQFVDEQDDPAFLLAQFV
 EDRLQAFLELAELGTGDQRPHVQGGQALVLEAVRHFAVDDALGQALDDGGLADAGFADQHRVVLGPPQLQDLGDPADLVV
 ATDHRVELAFLGALGHVDGVLVQRLARLLDVRVVRFAATQVGHGILQRLARHALAEQQLAEPGVLVHRGQQYQLAGDEL
 VALLLGQAVSLVEQACEILGQVHVAGRALDLRQVVEFFVEAAAQGGDIEADLHQQGLDRTALLLEQGGKQVHRLDGRMVM
 ANQOGLGVGERQLQLAGQTVYSHGSSFL*

>ORF23367 (SEQ ID NO:275)

ATAERLSSNPGRFRCWIRVSEARHFTDARGHVNPLIQKVLLFPRA TKRPFH CMRQSRAYRTPMKKPRRSGAFPVRPR
 RGQAKTISSPSTFAEILAPGANLPARISCASGFSIQRWMAFSGRAP*

>ORF25103c (SEQ ID NO:277)

SAPRGEHRRRDHRRGQAVAPLHRSATAGQHRPDRRGRQPHPHGDRLQAGGTGSSRPSPDPAEDRARGAEGRRRSHQ
 EAPGQAGGGYRQARARIRRPGRDLEVREGRGAGLGADPAEDRAGQAGDGGGAAQGRPREHGAHPVPDHPGPGTQPADGRP
 ARQDREPVAQQGDRRGNNRRSGFQVDRYPGVEDARGRAREAAAHGAGAASASDRPGRGGSSRRVQRRAPFARRPRRSEPAE
 RLVP LPRPDRGGQDRVVQAGRVPLRYRGAGADRYVRVHGETLGGPPDRRASGLRRLRGRRLPDRGDPQALLGGAAGR
 GGEPSGCIQHSPPGARGRTPDRQSRAYGGLPQHRGGDDLQPRFGADPGAGRRPRGATCRSDGRGQCALPSGIHQPDRRS
 GGVRAAGSRADRRHRRDPARSPAQAPGRARAEPGTEPGGAGQADCRLRPLGLWRTPAEAGHPALDREPAGATDPGRQIRA
 GCQYLGEGRRRDRRLRLTSSGADRESPASAGLFHGRPVGARALPHAVEGPF CRSWKKKNFLDQRVDMPARIRKMARL*

>ORF23556 (SEQ ID NO:279)

KSPA EAGLSL SAPEEVRRRSRRLPPSPRYWHPARICRPGSVAPAGSRSSAGWPASAGVRHRPGRSRRQSAC PAPPGSVP
 G SARARPGACAGDRAGSRRCRRSAREPAARTPPLRRSG*

>ORF26191c (SEQ ID NO:281)

KEGRPMRIDRLTSKLQALASDAQSLAVGHDHPAIEPVHLLSALLEQQGGSIKPLLMQVGFDAALRSGLNKELDALPKIQ
 SPTGDVNLSDLARLLNQADRLAQKGDQFISSELVLLAAMDENTRLGKLLLGQGVSRKALENAVANLRGGEAVNDPNVE
 ESRQALDKYTVDMTKRAEEGKLDPVIGRDDEIRRTIQVLQRR TKNNPVLIGEPGVGKTAIVEGLAQRIINGEVPDGLKDK
 RLLALDMGALIAGAKFRGEFEERLKAVLNELGKQEGRVILFIDELHTMVGAGKAEGAMDAGNMLKPALARGELHCVGATT
 LDEYRQYIEKDAALERRFQKVLVDEPSEEDTIALRGLKERYEVHHGVSITDGAIIAAKLSHRYITDRQLPKAIDLID
 EAASRIRMEIDSKPEELDRLDRRLIQLKIEREALKKEDDEATRKLAKLEEDIVKLEREYADLEEIWKSEKAEVQGSQI
 QQKIEQAKQEMEAAARRKGDLES MARIQYQTIPDLERSLQMV DQHGKTENQLLRNKVTDEEIAEVVSKWTGIPVSKMLEGE
 REKLLRMEQELHRRVIGQDEAVVAVSNVRRSRAGLADPNRPSGSFLFLGPTGVGKTELCKALAEFLDTEALVRIDMS
 EFMEKHSVARLIGAPPGYVGFEEGGYLTEAIRKPYSVLLDEVEKAHPDVFNILLQVLEDGRLTDSHGRTVDFRNTVVV
 MTSNLGSAQIQELAGDREAQRAAVMDAVNAHFRPEFINRIDEVVVFEPLAREQIAGIAEIQLGR LRKRLAERELSLELSQ
 EALDKLIAVGFDPVYGARPLKRAIQRWIENPLAQLILAGKFAPGASISAKVEGDEIVFA*

Fig. 4-12

>ORF23751 (SEQ ID NO:283)

TGSKPTAISLSSASWLSSRLSSRSARRLRRRPSWISAMPAICSRASGSNTTSSIRLMNSGRKALTASITAARCASRSP
ASSWICAEPRLEVITTTVLRKSTVRP*

>ORF24222 (SEQ ID NO:285)

PGGAPIRRATECFMNSDISIRTSASSVSKRNSASALHNSVLPTVPGPRKRNEPLGRFGSARPARERRTALDTATTASSW
PITRRCSSCSMRSSFSRSPSSIFDTGIPVHLETTSAISSSVTLRSNWFSVLPWSTICRLRSRSGMVWYWMRAMLSRSP
LRRAAISCLACSIFCWICAEPCTSAFSDFAQISSRSAYSRSSTLTISSSSLARRFLVASSSSFFSASRSIFSWIRRRSRRS
SSSGLESISMRMLAASSIRSMALSGSCRSM*

>ORF24368 (SEQ ID NO:287)

TRTYLSAPAPPRYRRGTRPAPCTTRSCPPRSGRGRGTSRSAGSDRRGRRANGARRWTRRLPPRPGRSLADAAPAPCAAAS
RARPRASSTPGYRSTWKPLRRFPRRSPCCAATGSRSCRAGRPSAGCVPGPGWSGTGCAPCSRGRPCAAPPSPAWPARSS
AGSAPSPAPRPSRTSRSPRGRIRARA*

>ORF24888c (SEQ ID NO:289)

RRKTTKPPGSAWPSWRRISSSSSANTFTSRRSGSPRRPRCRARRRSSRRSRPSRRWRRRGARATSRRAWRASSTRPSRTW
NAACRWSTSTARPTSCCATR*

>ORF25398c (SEQ ID NO:291)

RRSSTNWASRKAGSSCSSTNCTPWSAPARRKVPWTPATCSSRLWRAASCTASVLLPSTSIASSTRRMPRWSAASRRCWWT
NRARKTPSPSSVASRNMKCTTG*

>ORF25892c (SEQ ID NO:293)

PPGPAEGRPVHLQRAGIAGRDGREHQARQAAARPGRVAQGAGECRGQPAWRRSGERPERRGVAPGAGQVHRRHDQARRGR
QARPGDRSRRRDPPDHPGPAADQEQPGADRRTRRRQDRHRRGPGPAHHQRRSAGRPQGQAPAGPGHGGADRRCQVPRRV
RGTPEGGPQRTGQAGRPGHPVHRRTAHHGRRRQGGRRCHGRRQHAQAGSGARRAALRRCYPRRVSPVHREGCRAGAPLPE
GAGGRTERGRHHRHPPWPQGTG*

>ORF25110 (SEQ ID NO:295)

RSLRPRRMAMVSSSLGSSTSTFWKRRSSAASFMYWRYSSRVVAPTQCSSPRARAGLSMLPASMALPAPTVMVSSSM
NRMTRPSCLPSSLRTAFRRSSNSPRNLAPAISAPMSRASRRLSLRPSGTSPLMRWARPSTMAVLPTPGSPISTGLFLVR
RCRTWMVRRISRRPITGSSLPSSARLVMSTVYLSSAWRDSSTFGSFTASPPRRLATFSSALRDTWPWSSSLPSLVFSS
IAASNTSSLEMNWSPFCWARRSAWLSRRARSWDRTSPVGLWIFGSASSLLRPLRRAAISKPTCISRGLIEPPCCSSRA
ESRCTGSMAGWSWPTARDWASESASCSSLVKRSIRMGRPSFYRAGRNDGCP*

>ORF25510 (SEQ ID NO:297)

CAGPGPRRWRSCRRRVRRSAPGCSWSAAAAGPGWSGGSRRRDRSPGRACLPRAWSCRRCTCPAPGATPRRSGRSPLRHA
GWPRHSPAPCATRPGRAAACRAWCSRPSRPAIPARWR*

>ORF26762c (SEQ ID NO:299)

PPTACRRCSATARAPGWPRMPAGAGWRRACWRRRWTAWACPATNCWSGWGRRSARRPSRSAARSAMHSSLRTPRRARLS
YLAPIRAASWPTSTDGRSAWAPMASPPCMAAASAPSAIPRASIPTAARRVPAVLPAWSGSRTSPAQVIRRQLTDVTVRS
LEPRKIALIY*

>ORF26257 (SEQ ID NO:301)

IRAIFRGSSDRVTTSVSCRITCAGLVLEPDQAGKTAGTRRAAVGIEARGIAEGAEAAAMHGGDAMGAQADPRESVDVGH
EAARIGARYESRARLGVRSDCEIADLAADLEGLRADRRPQPDQQFVAGHAQAVHRRLQHARRQPAPAGMGRGHPGARAVA
EQRRQAVGGHDRTGDARHRAPAGVGPEHRFGSASTTSLRAPIPTSSAGIPDARSGVGGFIPRADRRRRGRQGSDCRRVP
G*

Fig. 4-13

>ORF26844c (SEQ ID NO:303)

RGGRPEPVLRADASWSAMPGVACTIMTADCLPALFCDSGTRVAAAHAGWRGLAAGVLEATVDSLGVPGDELLVWLGPA
IGPQAFEVGGFEVRDAFVAHAHAEARSFAVPSANPGRFMADIYRLARIRLGAHGVTAHVGGGCTFSDTARFYSYRRSSRTG
RFASLVWLQD*

>ORF26486 (SEQ ID NO:305)

MSAMKRPGLALGTAERASACAATNASRTSPPTSKACGPIAGPSQTSSSSPGTPRLSTVASSTPAASPRQPAWAAATRV
ERSQNNAGRQSAVMIVQATPGIALQLASALSTGSGRPPPRHSVHLFQPARPAFQTLGQASAVLFHGARIVVDVGAKVQTV
EGCLADPATARGHAGPHTGRRRPVGGQPGVQPTNASRSWRNRLSSQRNSSGSGDGHFMRTPVAG*

>ORF26857c (SEQ ID NO:307)

VHGVTTWRPTRTGAQGRRLERDAGRRLYDHRRLPAGVVLRLPLGHPGGRGPCRLARAGGGRAGGDDGGQPGRRRRRTAGL
AGAGDRPAGLRGRRRGPRCIRRCARRGALGFRT*

>ORF27314c (SEQ ID NO:309)

SGNRRCRKNSSGCSACCARIARRSSVERLADPRLAGAGPCAGLRDHAQWRGQPGTLRQSEPWRPRLRRSARRGIKPPTPD
RASGMPAELVGIGARSDVVEADPNRCSGPTPAGARCRASPVR*

>ORF27730c (SEQ ID NO:311)

QARRPGGPGSGCRPSGRHPAECLALPCPGHRQCAARRDRPPPGQGHDRPDGSGQDAGGPHQAGGATAGTVGQPHLRGDRDR
RDHLRRHRCADR TAWRAAAEDGGGRRRQGGGQPLPRAGTLP CAHPYPGQAGDRAYPPDPRAHEPYWLSPGRRSGLRWAL
QDSPGGQPDGPDSSRIPPAGAARALPRTGSPGHRAHEVGIAAAGRIPLAAQPVAPGSRGVRRLNAWLTPDWPAPARVR
ACVTTRSGGVSQAPFDSLNLGAHVYDDPRAVE*

>ORF26983 (SEQ ID NO:313)

PRHCAWSRRPAHGPPASRGSARRSTDERLAILAQQAEOPEEFFRQRRFPLHAHAGGRVIQFEEARVQRLPGEFAKSLDQ
GLAGHRGNPEAPTVDRIADQIGIANMAHVHADLVGTPGLQLDPGMGVRTEAFQHAVMADRHLAGVDHRHLLPLHAMPSDRR
IDGAAGGDHADHDLVDAADRPLQLRHQLGVGLQRLGHYHQAGRVLVQAVDDPGARHIGDVRDMVEQGIQQGAVLMAGS
RMDHQAGGLVNHQDVLVLVDDFQLDVLCEPLALGFLGLQDQLRAAVDDVARAQHGAVDGGQATVLDPAQGTGAGVFGKKL
GGDLVETLATQLERHLGRALNHIGHE*

>ORF28068c (SEQ ID NO:315)

PQRVADSKSRAEHRLLMSDMIQRAAEVPPFELGGQRLDQIAAQLFPEHSRSRLAGWIKDGRLTVDGAVLRPRDIVHSGAQ
LVLEAEQEAQGEWLAQDIELEIVYEDEHILVIDKPAGLVVHPAAGHQDGTLLNALLYHVPDIANVPRAIVHRLDKDTTG
LMVVAKTLEAHTKLVAQLQARSVSRIYEIVIGVITSGGTIDAPIGRHGVQRQKMAVVDAGKVAVSHYRVLERFRAHTHT
RVKLETGRTHQIRVHMSHIGYPLVGDPVYGGFRIPPVASTLVQTLREFPRQALHARFLELDHPATGVRMKWESPLPEE
FLWLLSLLRQDREAFVG*

>ORF27522 (SEQ ID NO:317)

PTPVAVAPPACWGPASWPLPSGRSCPCPGGGRSRAAHWRCPGHGRARHSAGCRPDGRQPDGPPGRRACQSPGCARPRR
RFPARCPVRATRPGLPARPPGPVARRCGRCRAGAARRRRRSGRDP*

Fig. 4-14

>ORF28033c (SEQ ID NO:319)

ASSPETHRYDSTRGRGAVRAGWPASRPDRRPAFSRTLPLPSGRLDQGRSPDRRRRRRAAPARHRPQRRATGPGGRAGSPGR
VARTGHRAGNRLRGRAHPGD*

>ORF29701c (SEQ ID NO:321)

SSSSLEISRTSTRPMVRRYRWYRRRMRCPCSSLSRSRSARTVALVLAQVRLAAIPALFVGEGVGLRHVDAAMGAADHRRRC
ARLVLRLLLLARS GTKATPEPERDGDQDPEQEA EKAHGD LGGWRKLQFSQAAGSIPDGKVQAVRRALGEAWRRRAKRR
EACASLRFCVRSVEETEGHVAPPATGVLVVIALLRLLVVGAVILVFRLQFGGDLPLGILVLLDHVLGGLGFHVRRRLAAF
DQAQGGGLQPGAGVGLAFAGDELAILEAGVIRIVQLEGFQAGAGQVETQATVGFDRQAIADGRGFLEVLHHVATAVG
GGDIGLALQVVVADVHFVGRQQVAQVHHARLGVRGVAAVGEAAGELGELVEGVAGGARVALGHVQRQEARQQA AVLVEGG
QAFEVGVVDVGLRMQADEAFGGGAGGFGLHVLVVGVDQLELGLLGVA AEG IARFEGFQLGDGAVVALVVEVVLRLLVQ
LALAQVLVDSLLVRGAGCGEGEDGDQQQVFHLHGGLRPWDGRLGLNRL*

>ORF28118 (SEQ ID NO:323)

QTVEAKPTVPGTQAAMQVKHLLLIAILALTAACSSNKETVDENLSESQLYQQAQDDLNNKSYNSAVTKLKALESRYPFGR
YAEQAQLELIYANYKNMEPEAARAAAERFIRLHPQHNPVDYAYYKGLSSFDQDRGLLARFLPLDMTKRDPGAARDSFNE
FAQLTSRFPNSRYAPDAKARMVYLRNLLAAYEVHVGHYYLKRQAYVAAANRGYVVENFQETPAVG DGLAIMVEAYRRLG
LDDLASTSLET LKNYPDNASLKDGEFVARESEADTRSWLAKATLGLIEGGEPPPHMETQA AKDVIKQYEDAEREIPAEL
KPENQDHSADDEKPESDDDEDGSRWSWSYMTFGLFD*

>ORF28129 (SEQ ID NO:325)

GQADRPRDASRHA SETPAADRHPRPHRSLLLEQDCRREP EREPAVPAGAGRPQQQELQQRHQAESPRIALSLRPLRRA
GPARADLRQLQEHGARSRRRRRTLHPPASAAPQRRRLRLPQRPVLLRP GPRPAGALPAAGHDQARPGRRLLRVRPA
HQPLPQQPLRPGRQGAHGVPAQPAAGLRSARRPLLPEAPGLCRRRQPRSLRGGELPGNPGRRRWPGDHGRSLSPSGSRP
GQHQPENPQAE LSG*

>ORF29709c (SEQ ID NO:327)

GPDLVWRWSAGVPVGRWSGGTGGTGGCVAPAPRS AVAVQ RARSPWSWRRCAWLQYQRC SWARALACGTWTPQWAQRTI
GDALGSSCGRCCWRGVGRVKRRQSQNAMAIRAIQNRKRPMVISEAGESCSLAKPPARSQTGRSRLCGVWRWERHGGGQ
KEGRPAPPFGVSCDQSKRPKVM*

>ORF29189 (SEQ ID NO:329)

SHETPKGAGLPSFCPPCLSQRQTPHSLDLPVWDRA GLAKLQLSPASEITMGLFRLLFWIALIAIAFWLWRRFTRPTP
RQQQRPDQEPSASPMVRCAHCGVHVPQANALAEHQRWYCSQAHLRQDQDRAR*

>ORF29382 (SEQ ID NO:331)

SPSRSGSGVALPVPLRASSNVRRTSRAHRRWSAAPIAASTCRRPTSPSTNNAGIAARRTCARTRATVRAERLRLSEEQOQ
RILRLYHLRLTIGLVLLISSELEDQVLKLVHPELFHVGSWCYLVFNILVALFLPPSRQLLP I FILALTDVLMCGLF
YAGGGVPSGIGSLLVVAIAIANILRGRIGLVIAAASLGLLYLTFFLSLSSPDATNHVYQAGGLGTLCAAALVIQALV
RRQEQTETLAEERAETVANLEELNALILQRMRTGILVVD SRQAILLANQAALGLLRQDDVQ GASLGRHSPMLMHCMQWR
LNPSLRPPTLKVVDPDGPTVQPSFISLNREDDQHVLIFLEDISQIAQQAQMKLAGLGRITAGIAHEIRNPLGAISHAAQL
LQESEELDAPDRRLTQIIQDQSKRMNLVIENVLQLSRRRQAEFPQQLDLKEWLQRFVDEYPGRLRNDSQLHLQLGAGDIQT
RMDPHQLNQVLSNLVQNGRLRYSAQAHGRGQVWLSLARDPESDLPVLEIDDGPGVPADKLNLFEPFPTTESKGTGLGLY
LSRELCE SNQARIDYRNREEGGGCFRITFAHPKRLS*

>ORF30590c (SEQ ID NO:333)

LLQQLGGVADRAQRVADLMGDAGGQAAKTGQLHLLRLGLDRNVFEEDQHVLVVF AVEADKAGLHRRAIRHHLERRRTEA
GIQAPLLHAVHQHRAVAAEAGALHVVLPEQAEGGLVGEEDGLTAIDHEDAGAHALQDQCEVFLQVGDRLGAFQGRFGLL
LAPHQSLDHQRGGEAQGA EAAGLDVVVGVRTAQAE EGGQVEQAEAGRRRDDQADAPAQQDVGNHRHHQQAADAAGYAA
TCVEQA AKHQHVGEREDEDRQQLPRRRQEQRDQVEDQVAPTADMEQFRVDELEDLIFQFAGDQDQYQADGQAVQVVT
EDALPLLLAQP*

Fig. 4-15

>ORF29729 (SEQ ID NO:335)

TVPCRQLVLPGLQHPGRAVPAAVAAIAADLHPRAHRRADALRPVLRWRRTQRHRQPAGGGGGHCQHFAAARHPGHRGG
GQPRPALPDLLPQPEQSGRHQPLRPGRPRHPVLRRRAGDPGSGAAPGADRNAGRRTRRDGRQPGGTQRIDPAAHHRHP
RGR*

>ORF30221 (SEQ ID NO:337)

PSGHPPRQPGRPRPAQAGRRAGRQPRPPQPDADALHEAMAPESQPPSADAQGGAGWPDGATQLYQPQPRRRPARADLPRR
HFADRPAGAADAGRSPDRRHRP*

>ORF30736c (SEQ ID NO:339)

SHSFRSSCCGSAWRRRESCTFSMTRFIRFDWSWMICVRRRSGASSSSSDSCSSWAAWLIAPSGLRISWAMPVRRRPRPAS
FICCACWAICEMSSRKISTCWSSSRLRLIKLGCTVGPSTTSLVGGRRLGFRRHCFMQCISIGLWRPRLAPCTSSCLSRP
RAAWLARRMA*

>ORF30539 (SEQ ID NO:341)

DPQAPGRDQPRRPTAAGVRGTGCPGPTPDADHPGPVEADEPGHRERPAALPSPPGRTAAARPEGVASAVRRRIPRQAAQR
QPTAPAARCRRHDPHGPPTVPEPGAEPGAERSSQLRPGARARPLAEPRARPGERPAGAGSHRRRSRRTGGQTEQPVRT
LLYYRKQRHRPGPLSLPRTLREQPGTDRLPQSRGRRRLPHHLRPPAQTQLTEAARMSRQKALIVDEPDIRELLEITLG
RMKLDTRSARNVKEAASCWPASRSTCASPTCACRTAAASIWSSTSSSAIHRPRWP*

>ORF31247c (SEQ ID NO:343)

FPAVRGYPVHRRRSGLVFGSCVRLPSAEFARVGEDEAEAAAFLAIIVVDPCLVALAEFAGEIEAQAGAFAFCSKEGFEQ
VVQFVRRYAGTVVDDFQHRQVALRVAREAQPDLAAPVRLGAVAKTVLHQVAQHLVQLVWVHAGLDVAGTELQVQLAVVAQ
PAGVFVDEPLKPLLQVELLRFGLAATGELQDVLDDQVHPLRLVDDLRLQASVRGIQFL*

>ORF30963c (SEQ ID NO:345)

LPAPAGRSPGRARGSARPGRARAPGRCSEDRSAPGCSAPGSTGVGPCSGCRRHRAAGAVGCRCACRGIRRRRTAEATPS
GRAAAVRPGGDGRAAGRSR*

>ORF31539c (SEQ ID NO:347)

GGCHQLPQATEVDRFGEEVEGTGLERLDRGVQAAVRGDHGRGLWMALLDVLDDQIEAAAVRQAHVGEAQVERLAGQQLAA
SLTLRALRVSSFMRRPVISSSSRISGSSSTIRAFCLMRASVS*

>ORF31222 (SEQ ID NO:349)

TGYPRTAGNHSRPHEAGHPQRQQRGSRELLAREPFDLCLTDMRLPDGSGLDLVQYIQQRHPQTPVAMITAYGSLDTAIQ
ALKAGAFDFLTKPVDLGRRLRELVATALRLRNPEAEEAPVDNRLLGESPPMRALRNQIGKLARSQAPVYISGESGSGKELV
ARLIHQGPRIERPFVPVNCGAIPSELMESEFFGHKKGSFTGAIEDKQGLFQAASGGTLFLDEVADLPMAMQVKLLRAIQ
EKAVRAVGGQQEVAVARAHPLRHPQGPRRSRRRALPPGPLLPPQRHRAARTPLRERREDIPLAERILKRLAGDTGLPA
ARLTGDAQEKLNRYRFPGNVRELENMLERAYTLCEDDQIQPHDLRLADAPGASQEGAASLSEIDNLEDYLEDIERKLIMQ
ALEETRWNRTAAQRLGLTFRSMRYRLKKLGID*

>ORF31266 (SEQ ID NO:351)

SWTPAAPATSRKPRVAGPRAVRPVPHRHAPAGRQRPRSGPVHAPAPSTDPGGHDHVRVQPGHRDPGAQGRCLRLPHQTGR
PRSLAGAGGNRPTLAQPGSRGSAGGQPPARRVAADARPAQPDQAGAQPGAGLHQWRVVRQQTGGAPDPAGATYRAAV
RAGELRRDSLADGKRVLRPQERQLHWYRQAGPVPGRQWHPVPRRSRRPADGHAGQTAPGDPGKGRARGRRPAGGRR
RTCASSAPPTRTSPPKSAPGASARTSTTASTSSSCAYTAARTPRGHAPARRTHPQAPGRRHRPAGRQADRRRTGEAEELP
LPGQRPRAGKHAGARLYPVRPPDPASRPAPGRCAGCQPGRRREPERNRQPRGLPGRHRAQADHAGTRGDPLEPHRRGPA
PGPDVPLDALPPEKAGHRLKVKRPVRRQAFWFSLLRGDQPGRRGPR*

>ORF31661c (SEQ ID NO:353)

TGAWLRASLPWLRRARIGGDSRRLSTGASSASGLRKRRAVATSSRKRPRSTGLVRKSKAPALSAWIAVSRLPYAVIM
ATGVCGWRCWMYWTRSRPLPSGRRMSVRHRSNGSRASNSRLP*

>ORF32061c (SEQ ID NO:355)

RSWRKRPAPTSAAARSLWVAQRMRTCDGDLALLAADRAHGLFLDRPEQFDLHGHRQVGDFVEEQGATAGGLEQALLVFDSAS
EAAFLVAEELAFHQLGGRNRAAVHRHERPLDTWPLLVDOARHQFLAAAGLATDVRRLAARQLADLVAQGAHRRRLAEQAV
VHRRFLGFRVAQA*

>ORF32072c (SEQ ID NO:357)

GGSRGPGGSARRRLRRRGPCGWRRGCARATATSCWPPTARTAFSWIARSSLTCAIGRSATSSRNRPPLAAWNRPCLSS
IAPVKLPFLWPKNLSISSEGIAPQFTGTNGRSIRGPCSWIRRTATSSLPLPDSPLM*

>ORF31784 (SEQ ID NO:359)

WKASSSATRKAASLALSKTSRACSRPPAVAPCSSTKSPTCRWPCCSNCSGRSRKRPCARSAASRRSPSHVRILCATHKDL
AAEVGAGRFRQDLYYRLNVIELRVHRCANAARTSRCSPNASSAWPATPACRPPG*

>ORF32568c (SEQ ID NO:361)

GAKTKRPVFGQAFSLSVDAQLFQAVAHRAERQAQALGRGGAVPAGLLECLHDQLALDVFQVVLEVVDFAQARGAFLAGTR
RIGQAQVVRDLVVFAQGIGALQHVFLADVAREAVVLQLLLCVAGQPGGRQAGVAGQALEDAFGEQRDVLAAFAQRCTR
SSMTLRR*

>ORF33157c (SEQ ID NO:363)

TDGGARLVARRRSSGRRGLAWRDPWRQGAAGGRRLERRVVEAAWPGTARGTGERSDDPLQVRGGFPAAHGAGQGALRDS
AARRPHPDRLQHLGTFGLRQDADRRGAGKPQGVCGRTVAGTGGHAAGGPLGRVAPGLSRRHPLYRSGAWLRRALAEYRALP
QRAGPGTGVVPSAGGSHERAGTDHRPGPLRPGWSPLRSENQACLTGLFTFSRCPAFSGGSASSGTSGPGAGPRRCGSS
GSPRVPA*

>ORF32530 (SEQ ID NO:365)

KGLSEDRPFGFRSSEATSRGVGGRVDDRFPFAHEIRQQTARRRCQDQPVAVVPGIQPEPVEARHRTDIGDAFGRARAQPC
PVGHRHLVRQFRQQFCRRRPEAFQRLVGRRLVEARMFQGAADQDVAVAPRNRVAPLQGHARQEIRRALVEDHLTFHRYH
GQFQAKRLQQLAAPGACRQQLVATDLATRGRHADHSIAVAQPAHLRLFMQLEIGELLQGCPCQ*

>ORF33705c (SEQ ID NO:367)

VIFLCWQIGRSPVVS RDVVVGAGVIGLLTARELALAGLRVTLVERGESGREASWAGGGIVSPLYPWRYSPAVTALAHW
SQDFYPALGQRLLEDGLDPEVHTVGLYWLDDQTEALQWARNHTRPLKEVPIEEAYA AVPGLGAGFQRAVYMSGVANV
RNPRLARSLRASLQQFANLELHEQTEVRGWL RDGDRVVG VATSRGEIRGDKVLLAAGAWSGELLKPLGLELPVVPVKGOM
ILYKCAADFLPRMV LAKGRYAIPRRDGHILIGSTLEHSGFDKTP TDEALES LRASAAELLPELADMQPV AHWAGLRPGSP
EGIPYIGPVPGFDGLWLNTGHYRNLVLAPASCRL LADLMSGREPIIDPAPYAPAGRL*

>ORF32832 (SEQ ID NO:369)

GFPAPRRSASCSPNVPRCCRSGCGRRAAESRSAPWPAPCAAGNPRTCRGSSDLSVPVRAVPQGAASTTRRSRRLPPAA
PCRHSRHRASPRRPLDRRRATSRA PPSVHATRDWRIVAGMPAMSAPGEDCAHWPRPTCRPPAGSLRPARAPRRPPRSA
LPSTAGCGCVPTAVPRSGRPGPASTGQRYGPRDRARSRRANAAPGPGRSPATSAPGRSPPGCSATDRAARRSRLPPRMPH
AHSRPAPPGPSAVRRAPAPGRSTGR*

Fig. 4-17

>ORF33547c (SEQ ID NO:371)

GILGGRDRLAALSVALQPGGDRPGALVAGLLPGPGAFAARRDRARSRGPYRWPVLAGPGRPDRTAVGTQPHPAVEGSA
DRGGLRGGARAGRRLPAGGLHVGRGQCAQSSPGALIAGIPATIRQSRVA*

>ORF33205 (SEQ ID NO:373)

ARQARIAHIGHARHVDRLPACAPGHRRVGLDRHFLQRPVVACPLQCLGLVVQVQPVQANGMDLGIEPGLVEQTLPO
GRVEVLRPVRRQGGHRAVAPRIERRDDPASRPGCLTPTLAPLHQGHPOSGERQLPGGQQADDASAYHYIISTHHRAPTDL
PGTEKYHSGSDADELPASTNSVESSPGEKPIPAEVFIP*

>ORF33512 (SEQ ID NO:375)

SGETIPPPAQDASRPLSPRSTRVTRSPASASSRAVNRPMTPAPTTTTSLTTGLLPICQEQRNITQRDQMLTNCLLQRTQ
SNLVPVKSPSPQRYSSHEIEWFEFGGTIDSPIDPCDRRDNCAAHPPRQNEAGH*

>ORF33771 (SEQ ID NO:377)

KAHHTRRGIHPMKSSGLNLVELSIVLSILAIGVTIALPTLPDRMKRDISRDIGSLTSHVMAARASSIQNGVIIIEVCGSG
DGSTCSEEWHLGWFSRNDRSQILARHENTSRTDIHWRGFDKRLRYLPNGTSPTGNRFFECKDDRIEWQLVLNRQGRRLR
VAGSENKKLSYLCSSR*

>ORF34385c (SEQ ID NO:379)

WRAHCPCSRDSRSGEWDWQTVCTVLSPPGAQVRELFIFALSRHPEALPIEQHQLPLDAIVLTFEETPVTCRAGAIRQV
AQSLVEAPPMNIGATRIFMPGQYLLAPVVTAEPAMPFLAAGTAVTATAHLDDHAVLYAASPRSHMTSQAVTNITANVP
LHSVGEQGRNCHAYRKDR*

>ORF33988 (SEQ ID NO:381)

SSRCAVAVTAVPAARNGISAGSAVTTGANRYWPGMKIRVAPIFIGGASTSDCATCLMAPALQVTGVSSNVRTIASSGNWC
SIGKAASGWRERAKIKSSLTCAPEGGERTVSHTVCSHSPRLRLSLQGCALH*

>ORF34274 (SEQ ID NO:383)

KALLPVLQAVRELFHIPFASHPTLRSGCLCYRDNALSTRQDYALFLVEYCMRSICRSAGFSLIELMMVLVLVAIFASIA
VPSFNALIERNRIQTASEELYSLLQYARSEAVNRHANVSIRATQNDWAKGLEIISGATTVQKHQGFQQVSLSSASSATAE
LTFNATGTLNSQAANIDIKVCFAGDKSTGRLLTVQPSGRVILYPPSSKQPDSCN*

>ORF34726c (SEQ ID NO:385)

RDLETLVLVLLHGGAADDFQAFCPVIVLRRPDAHIGMTVYSFAASVLKQAVEFLAGSLDSVALDQGVETGYGNAGEYGDQ
NQHHHQLDQKGAGAAATNRAHAVLHKEKGQIILPSGERIVPVAETAGAESGMTGKRYVKQFSHRLEHR*

>ORF34916 (SEQ ID NO:387)

GKPMSRETGFMSIEVLVALVLISIGVLGMVAMQGRTIQYTQESVQRNAAAMLASDLMEIMRADPDAVLNLRALREDSVY
YKAKGSDFPAPARCAPLPADAKERLGCWAQQASKDLPGASALLNSQFYICRSPTPGTCDNTKGSATIEIQVAWRAMDGAC
FNASDSTLCTYSVRSEL*

>ORF35464c (SEQ ID NO:389)

RACLFSGFADAVGAQGGVGRGVETRSIHGSPGNLDFDGRAFGVVAGTRGWAATNVELAIQECGGSRQVFRGLLGPAETP
LSICQWRAARWGCGKVAALGLVVDVFA*

>ORF35289 (SEQ ID NO:391)

IANSTFVAAQPRVPATTPKARPSKRLPGEPWMERVSTPLTPPCAPTASAPNCENKHALQQNAERPIDGRTARGTRYKQL
PDPGDQPDHLRQQTQLSFPARPGRQPGK*

Fig. 4-18

>ORF35410 (SEQ ID NO:393)

LHLVHLQRPLRIVRTSMLFSKMQKGLSMVELLVALAISSFLILGISQIYIDNKRNYLFQQGQAGNQENSRFVLMMLQQQL
DKTAYRRLHDDNMENAFKSATFNGCRAVAGETIAAATALKAGEYGVCLRYQPAYKGEHDCLGNEITGVPEKPFNTTPPV
VVRVLVYLPAGTLCSCRPDIAQSKSGELVSGLTDFRLEAGVGPADRSEKRVSSFVALQDVAGRPILALRFSILAGSDNTS
LRTGDDSQARDRWIVLYPESKSAIEADKGOIYQIARGNQITIRNLMP*

>ORF35907c (SEQ ID NO:395)

VDQANDDRGSICEGLFRNSGNFITEAIMLPFVGGLIAQADTVLTRLLEGSCRSDSLASHKCTTAIECRGFESILHVVVVKA
TIGCLIQLLLQOHKNEAAIFLVAGLALLEKIVAFVVDVLDADPQDQEAAYSECHEQFYHR*

>ORF35534 (SEQ ID NO:397)

SWGSRSTSTTNATIFSSKARPATRKIAASFLCCCSNNWIRQPIVAFTTTTWRMLSNPRHSMVHLWLARLSLRQLPSR
RVSTVSACAINPPTKGSMIASVMKLPEFRKSPSQILPLSSFAWSTYRAPVP*

>ORF35930 (SEQ ID NO:399)

VAVVPISPSRNRENWSVVSQTSAWKRGSGQQIVANAKYPASSHYRMSPVVLSEHCASQSWQAATIQACAQEMIARHAIAG
SSFIPRAKAPSRPQTKARFTK*

>ORF36246 (SEQ ID NO:401)

PNHQESHAMTLRHTSRQOGSTLLISLVILLMITLLAVSNMREVSLESRITGNLIEQKRLRNAGEAGLREGERRFFNTIKP
PEVGS GCADSNVKRPCILNLSALSVPRDDVHNNPVAALNGKTDNANSRVWMPYRGSDLNNPTQIDKDRAVTWQTITVPAG
EQNNEAENPEYGNMMRGVGTFFYYETNSRALNKAGGETVLQAVHARLYTN*

>ORF26640c (SEQ ID NO:403)

GIQTRELALSVLPFRAATGLLCTSSRGTERALRFSMQGRLLTLLSAHPLPTSGGLMVLKKRRSPSRSPASPALRRRFCMR
LPVIRLSSDTSRMLETARSVIINKITSEINNVDPCCREVWRRVMA*

>ORF36769 (SEQ ID NO:405)

CAGSARSTTKPTAAPSTRRAERLFYRPFMHACIPTDWSQRMHQITRAGKSLAAGCTLSILFASDSYAATALNVSQQPL
FLTQGVAPNLLFTLDDSGSMWAYVPDGISGNSGRAGRSSDYNALYNPDIYAYQVKKLTLSGDQIIVSDYPVPRFTA
QDGYAQGSTTNLSNNYRPQWGTGWLGCIDSSCNTGRAYYYTYKVSASCPAQPVSSNSCYTYNALPTSQESNF
AIWYSYRNRILATKTAANLAFYSLPENVRLTWGALNTCSIGANSRSCONNALLQFNKQHKINFFNWLANS
PASGGTPLHAALDRAGRFLQTNGTAYTTEDGKTYSCRASYHIMMTDGIWNGRNVTPGNLDNQNTFPDSTLY
RPPYADSNASSLADLAFKYWTTDLRPSIDNDLKPFMAYKSGDDSKDYWDPRNNPATWQHVMNFTVGLGLSYSL
TLNSAPTWTGSTFGNYEELMAGSKAWPSVDNDAAPGNVYDLWHAAINSRGDFFSAESPSLVQAFNKIL
TRISERNSTSSSKPAMTSALQDDGTGDKLIRYSYQSSFASDKNWAGDLIRYKVESTSTGSKTQ
EWSAGALLDNRAPATRNIIYASNSGTNRLLKPFWSNIEGSQLATWLNRPDKDNQADTKGAQRVDFIR
GQQNMDGFRQQAVALGDIVHSSPAVVGPAQYLTYLANPIEPSGDYGTFFKTEADQSRPRVYVGSNDGMLH
GFNIKTGVEEFAFIPTAVFEKLNKLTGISYQGGAHQYFVDATPVVSDAFFDGAWHTVLIGTLGAGGRGL
FALDVTKPDDVKLLWEYDSSDSDLGYTFSKPTVARLHSGQWAVVTGNGYGSNDKAAALLIDLKKGT
LIKKLEVQSERGIANGLSTPRLADNNSDGIADYAYAGDLQGNIRWFDLIGNTRNDPDNTSINPFKPGD
VPSAFRVSFSGAPLFRARADNNTROPITAPPTLVRHPSRKGIVIVGTGKYFEDDDAQADTSRAMTLYGI
WDRQTKGESANSTPTIDRNALTAQMTTEANSTFGSVNRNIRLISQNPVKWYKDGATGTANS
DVASYGWRNLNEVNSSKKGEMMIEDMFAAGQVLLQLTLPNDPCDSGSTSWTYGLNPYTGGRTSFTV
FDLKRAGIVDSGSDYNGSVSAFQQDGLGGLAITQNEQRQSEACTGDECIIFNPSDKSNGRQTWRVVEEK*

>ORF37932c (SEQ ID NO:407)

AGIAVGIRGLWPPIEGAIRKGLVLVVEIAGGDVPTVPDTPVGHHDVIAGPAGICLSVFGGISC
AVGLQEASGSVKSARMQRSTAAGRAVRQPIEIDFVLLVELEQGIVLAASAVGADATGVQGP
PSETHVFRQAVKGQVGSGLCGQDAVAIVGVPRKVAFLTGRKSIVGITVGAAHRLCRAASAY
LISIVISSPGIAAAIDATKPAGSPLRAIVIAQVGGGALGVAILPGCEAWHWIVGNDDLIA*

Fig. 4-19

>ORF38640c (SEQ ID NO:409)

LTSLNIPACERLKAVGSAIAGDVNITGSGSSVVQQCAGAPFLGFGRTGGSRLHLVTKVARPVLVTGKAGLVAVADQLVA
GSVILQRGSHCWFGGGGVALGNPCQDLIESLNQRVR*

>ORF39309c (SEQ ID NO:411)

SCLVIIASIAVAGNYCPLSAVQSGYGRFEGVTKVRVGTAIVFPKQLDIVRLGYIECEQAATSSTKRSDQNSVPSSIEKG
IADDRCSVDEILVGTALVADAGKLVKLFYCCRDESELFHAGFDVETMQHAIVGSNINSRAALVCLCLECAVVAAGFDGV
GQISEVLGRSDHGWRVRVHDVP*

>ORF38768 (SEQ ID NO:413)

GTSCTRLQPWSDRPNTSLIWPTSPNPAATTAHSRQRQTSAALEFMLDPTMACCMVSTSKPAWKSSLSLQQYKSLTSLP
ASATRAVPTNISSTLHRSSAMPFSMELGTLF*

>ORF40047c (SEQ ID NO:415)

KHLAGSEHIFDHHFAFLAIDLQIQSPAIAASHIRVRGTGCSVFVPLHRVLANKPNIPVHATECGVRLCCHGLGCEGVAVD
GWGTVCAFALGLAIPDTIERHGSAGIGLSVIVLEVFSCTYDDVALTARMAYQGRSRDGLTSIVVGASTEKRGAERYS
ESRRIYISGLEIDRGICVWVVVAGIADQIEAPDISLQIASIGVVSNAIAVVISQARRR*

>ORF40560c (SEQ ID NO:417)

PASPVVGHGWASDMSAHRLLPDRRQDEHPRPRPHSRITYSWHSRQRLGKPELELQELWREDVRGSCSFLDDPPGLSSVTL
VAGVEDDALITSASLGLTLFVLGNGQAT*

>ORF40238 (SEQ ID NO:419)

VAWPLPRTNSVNPRLALVMSASSSTPATRVTDKPGGSSRRNEHEPLTSSRHSSCSSSSGLPNLCLECHEYVRECGRGRG
CSSCRRSGSSRWADISLAQPCPTTGLAGHILGTSGTDSVFLRQTHQRPARNRVVLHYQAGPSRSLRIGAATMKSNRGFTL
IELMIVVVIIAILAGIAYPSYDEYVKRGNRTGQALLSEAAATQERYFSQNTYITTQADIGKLHMRNTSGTTVKSSSTGK
YSLTVDTVANDGGYRLIANQAFNDLDCGNLTLTANGEKGRTGSKKSVAECWR*

>ORF40329 (SEQ ID NO:421)

RTTNLAGRRGEMNMPLRLLATALAALALACPTFALSATNTFENVGVVEDVHPAAGLVVVDGQTYRLPNRVQQQDSPVIF
LVRQGQTVSFSGLTSDLPEIESFYIIKQAPLVPFGSEQQQ*

Fig. 4-20

>ORF40709c (SEQ ID NO:423)

SLCSTSLLLLRSEGNERGLLDNVERLDFWQVAGEFAGERHCLSLTYQEYDRRVLLLDTVGQAIICLPIDYYQTGGRMNILD
HAHLERIRGTQKGWASQS*

>ORF40507 (SEQ ID NO:425)

SMGRHIACPTVSNRTRRSYSWYVRDRQCLSPANSPATCQKSSRSTLSSRPLSFPSDRSSNNEVEQRLHSHRVDDRRSNH
RYSCWYRLPQLRRIREARESHRRTGITQRSSRYSRALFFTEQYLYHYPSRHRQAAYAQHIGHHSEVLHRQIQPYRRYGSQ
RRRLSPYR*

>ORF41275c (SEQ ID NO:427)

VGGVGRAGTGGTGGEHYLLDAQGTAGQGFVIGIFAHLLKKPGLCRALPFSCLGALAPAFCNALLASSPAFLAVGGQGQVAT
IKIVECLVSDKAITSVVGYRIDGKAVFACGGLHCGARCVAHMQLADVGLGSDISIVL*

>ORF42234c (SEQ ID NO:429)

STSSRPEPSVAAPFPSGEGGSKVHSSNHRVAHETAMQIKLANPRGFCAGVDRAIEIVNRALDVFGPPIYVRHEVVHNFV
VDNLRQRGAI FVEELDQVPDNVIVIFSAGVVSQAVRKEAEGRLKVFDATCPLVTKVHMEVVRYSRDGHECVLIGHEGHP
EVEGTMGQYDASNGGAIYLVDEADVAALEVRKPEALHYVTQTTLSDMDTSKVIDALRAKFPQIQGPRKNDICYATQNRQ
DAVKELADQCDMVLVVGSPNSSNSNRLRELAERMGTPAYLIDGAEDMQRGWFDGVERRIGITAGASAPEVLVRGVIAQLRE
WGASEEQELEGREENITFSMPKELRVKAL*

Fig. 4-21

>ORF41764c (SEQ ID NO:431)

RPPRGGRHHGVPVRCQQRCHLPGGGRGRRRRAGGAQARSPALRDPDHPVDGRHLEGHRCPARQVPADPGAAQERHLLCHP
EPPGCREGTGRPVRHGPGGGQPOQFQLQPPARTTAAHGHAGLPDRRRRGHATRLVRRCASHRNHRRRLRAGSAGARSDRP
AT*

>ORF41284 (SEQ ID NO:433)

LGDHSAHQHFRRGGACGSDATHTVEPAALHVLGAVDQVGRRAHALGEFAQAVGVGTVGAAHHQDHVALVGQFLHGILAV
LGGIADVVLARPLDLRELGAQGIDDLRGVVHRQGGGLGHVVQGFGLAHLQRGDVGLVLHQVDGTAVAGIVLAHGAFHLGVA
FMPDQHAFVAVAAVAHHFVHLGHQRAGRVENLQAAPLGFLADRLGNAVGAEDDDVVRHLIEFLDEDGAALAQVVHDEL
VVHHLVTHVDRRAEDIEGTVDDLDGAIHAGAEAAGIGFDLHGGLVGDAVIGRMNLATALPAWEGRSDDRRFRPAGRR

>ORF41598 (SEQ ID NO:435)

PSRCRPSTGWSGSRSLACAPPARRRRPRPPPGRWHRRCWHTGWPCLPPRGGLHARSARIRGRRGCSAPLPCAPWSP
AGRSRRKPSGRAPRLPCGPPGKRRGR*

>ORF42172c (SEQ ID NO:437)

QGSFVQSPRRPRDRHANQTRQSPRLRRRGSRRHRDRQPCPRCLRPADLRASRGGAQQVRRGQPAPARRHLRRGTRSGAGQ
RHRHLQRPRRFPGGPQGSRGARPEGFRDLPAQDQGAHGSGALQPRRPRMRADRA*

>ORF42233c (SEQ ID NO:152)

RRPAGLNRRSLRPSQAGRAVARFIRPITASPTRPPCKSNSPIPAASAPAWIAPSRSSSTVPSMSSARRSTCVTRWCTTSSS
WTTCAAPSSSRNSIRCRTTSSSSSAPTAFPRRSARKPRGAA*

Fig. 4-22

33A9 (SEQ ID NO:102)

CAAAGCATAAGACCAAGATGGCACATTGCCAACAAAATACCCTTCCCCGCTACCGTTGTTTTATCGTTGTTGCCAGCCCT
 GATCTGGCGGAAAAGCCCGCTCCATGAATCGTCATGGAGCCTCCCATGTTTCAACTCCTTTCTGGATATCCAGGAAGCC
 GTCCCCACCCCAACAACCAAGCTGCCCCAGGGGGATTATCCTTCTCTGAGCAGCATGGAAGTCTCGGCACGCCTC
 GCGCGCGCAGCTACTGGAGAACATCTGGCAGCGCGCCTCGCTATCCAAGCAGCAATTCGAGGAGATCTACCGCGGCCA
 CTGGCCAACTATGCCGAGCTGGTCCAGCAGCTCCCTGCTTCGGAAAATCATCACCATGCCCATCCAGGCGGGATGATCGA
 TCACGGCCTGGAGATCGTGGCCTACGCACTCAAGGTACGGCAGACCTACCTGCTCCCGATCGGCGCAGCGCCGGAGTCAC
 AGTCAGCCCAGGCTGAAGCCTGGTCGGCCGCCGCGCGTATGGCGCCCTGGCTCATGACATAGGCAAGATCGTCGTCGAC
 CTGCAGGTTGAGCTACAGGACGGCAGCACCTGGCACCCCTTGGAAACGGACCGATCAACCAGCCATACCGCTTCAAGTACGT
 GAAGTCCCGCGAATACCAGCTCCACGGCGCTGCCTCAGCACTTCTCATCCACCAACTGCTACCGCGCACTGCACTCGATT
 GGCTCAGTCGCTTTCCAGAGCTGTGGGCTCAATTGATCTACCTGTTGCTGGGCAGTACGAGCAGCGCCGGGATCTCGGC
 GAGATCATCGTGAAGGCAGACCAGGCCTCAGTTGCACAGGAGCTAGGAGGCAATCCGGATCGAGCTCTGGCTGCACCGAA
 GCAGTCGCTGCAGCGGCAGTTGGCAGACGGCCTTCGCTTCTTGGTGAAGGACAAGTTCAAGTTGAATCAACCTAGCGGCC
 CGTCTGATGGATGGCTGACCCAGGACGCACTCTGGCTGGTGAGCAAGCCTGCTGCCGATCAACTGAGAGCCTACCTGCTG
 GCCCAGGGTATCGATGGGGTGCCCTCCTCTAACGCGCCGTTCTTCAGCATGCTCCAGGACCAAGCCGTATCCAGACAAA
 TGCCGAGGACAAGGCCATTTGGACGGCCACGGTAGACAACGGTGCTGGATGGAGAAACAAGTTCACGCTACTCAAGATTG
 CTCCAGCCTTGATCTGGACAGATGCTGCCGAGCGCCCTCACCTACAGCGGATCACTGGTCTGTAAGATGGAACCGCC
 TCAACGGAAAAGCCGAAACGACCTGTGAAATTCCTAACGGGCCGGCTGAACAGCAGCAAGCACCAGAAACGAAGATGAT
 GCTCCATCAACCTGCGCCGAGCGTTGCGAAACCGGCAACGAGACGCGAGGCGATTGCGAAACCTCAACTGATGATCAAG
 AAGAAACAGACGATTTGTATGCACTTCTTGGTAATATCAATTGCGCACTAGAAGAGCTAGACACTAGCCACGACTCGCCG
 GCTGCCTCTCCTACGAACACACGCGGGGAGGAGAACCTACAGCAGCCACTAGGGACCAAGGAGCCAACAGATTGCGCTCC
 TGAAGCAATTGAAGATGTATTTATGCCTAGCAGAAGTACTGATCTGGGACAGGGATTGTTGGTTGGATGAAATCTGGCA
 TCGCGGCGCGTCGCTGTTTCATCAACGACACCAAGGCTTTGGTGCATACCGTAGACGGGACCGCCATGCTGGTCAAGCCA
 GGAATTTTCAAGCGCTATGTCCAAGAGCATCCGGTGCTTGAAAACTGGCCCAAGCCAAGGAGACGACCGGCTGGAAGCT
 GGTGCAGCGCGCGTTGAAAAACAGGGGCTTCATCGGAAGACCAGTAAAAACCTGAACATCTGGACCATCAAGGTTTCTG
 GTCTTCGCAAGACGAAAGAGCTCAAGGCCTACCTGCTCCAGGATCCCAAATTGCTGTTCCCTGAGCAGCCTCTGGACAAC
 CCAAGCCTCACGGTCATCACCATGCCGAAGGAGGTGTGGAATGACGCCGAGCAGCTCACCAGGAGTACATCTTCGCG
 CACGATCTCCGGGAAGCCAGC

Fig. 5

33A9 SEQ ID NO:103

1 MNRHGASHVS TPFLDIQEAV PHPNNQSCPR GIHPSSSEQHG TARHASPPAA
51 TGEHLAARLA IQAAIRGDL P AATGQLCGVG PAxPCFGKSS PCPSRRDDRS
101 RPGDRGYALK VRQTYLLPIG AAPESQSAQA EAWSAAAAYG ALAHDIGKIV
151 VDLQVELQDG STWHPWNGPI NQPYRFKYVK SREYQLHGAA SALFIHQLLP
201 RTALDWLSRF PELWAQLIYL FAGQYEHAGI LGEIIVKADQ ASVAQELGGN
251 PDRALAAPKQ SLQRQLADGL RFLVKDKFKL NQPSGPSDGW LTQDALWLVS
301 KPAADQLRAY LLAQGIDGVP SSNAPFFSML QDQAVIQTNA EDKAIWTATV
351 DNGAGWRNKF TLLKIAPALI WTDAAERPSP YSGSLVVEDG TASTEKPETT
401 CEIPNGPAEQ QQAPETKMML HQPAPSVAKP ANETQAIAPK STDDQEETDD
451 LYALLGNINS PLEELDTSHD SPAASPTNTR GEENLQQPLG TKEPTDCAPE
501 AIEDVFMP SR STD LGQGFVG WMKSGIAARR LFINDTKALV HTVDGTAMLV
551 TPGIFKRYVQ EHPVLEKLAQ AKETTGWKLV QRAFEKQGLH RKTSKNLNIW
601 TIKVSGPRKT KELKAYLLQD PKLLFPEQPL DNPSLTVITD AE*

Fig. 6A

33A9--ORF1 SEQ ID NO: 189

ATGGAGCCTCCCATGTTTCAACTCCTTTCTGGATATCCAGGAAGCCGTCCCCACCCCAACAACCAAAGCTGCCCCAGG
 GGGATTCATCCTTCCTCTGAGCAGCATGGAAGTCTCGGCACGCCTCGCCGCCGAGCTACTGGAGAACATCTGGCAGC
 GCGCCTCGCTATCCAAGCAGCAATTCGAGGAGATCTACCGGCGGCCACTGGCCAACTATGCCGAGCTGGTCCAGCAGCTC
 CCGCTTCGGAATAATCATCACCATGCCATCCAGGCGGGATGATCGATCACGGCCTGGAGATCGTGGCCTACGCACTCAA
 GGTACGGCAGACCTACCTGCTCCCGATCGGCGCAGCGCCGGAGTCACAGTCAGCCCAGGCTGAAGCCTGGTGGCGCCCG
 CGGCGTATGGCGCCCTGGCTCATGACATAGGCAAGATCGTCGTCGACCTGCAGGTTGAGCTACAGGACGGCAGCACCTGG
 CACCCTTGGAAACGGACCGATCAACCAGCCATACCGCTTCAAGTACGTGAAGTCCCGCGAATACCAGCTCCACGGCGCTGC
 CTCAGCACTTCTCATCCACCAACTGCTACCGCGCACTGCACTCGATTGGCTCAGTCGCTTCCAGAGCTGTGGGCTCAAT
 TGATCTACCTGTTGCTGGGCAGTACGAGCAGCGCGGATCCTCGCGAGATCATCGTGAAGGCAGACCAGGCTCAGTT
 GCACAGGAGCTAGGAGGCAATCCGGATCGAGCTCTGGCTGCACCGAAGCAGTCGCTGCAGCGGCAGTTGGCAGACGGCCT
 TCGCTTCTTGGTGAAGGACAAGTTCAAGTTGAATCAACCTAGCGGCCCGTCTGATGGATGGCTGACCCAGGACGCACTCT
 GGCTGGTGAGCAAGCCTGCTGCCGATCAACTGAGAGCCTACCTGCTGGCCAGGGTATCGATGGGGTGCCTCTCTTAAC
 GCGCCGTTCTTCAGCATGCTCCAGGACCAAGCCGTATCCAGACAAATGCCGAGGACAAGGCCATTTGGACGGCCACGGT
 AGACAACGGTGTGGATGGAGAAACAAGTTCACGCTACTCAAGATTGCTCCAGCCTTGATCTGGACAGATGCTGCCGAGC
 GCCCCTCACCTACAGCGGATCACTGGTCGTTGAAGATGGAACCGCTCAACGGAAGCCGGAACGACCTGTGAAATT
 CCCAACGGGCCGGCTGAACAGCAGCAAGCACCAGAAACGAAGATGATGCTCCATCAACCTGCGCCGAGCGTTGCGAAACC
 GGCAAACGAGACGCAGGCGATTGCGAAACCTCAACTGATGATCAAGAAGAAACAGACGATTTGTATGCACTTCTTGTA
 ATATCAATTCGCCACTAGAAGAGCTAGACACTAGCCACGACTCGCCGGCTGCCTCTCCTACGAACACACGCGGGGAGGAG
 AACCTACAGCAGCCACTAGGGACCAAGGAGCCAACAGATTGCGCTCCTGAAGCAATTGAAGATGTATTTATGCCTAGCAG
 AAGTACTGATCTGGGACAGGGATTCGTTGGTTGGATGAAATCTGGCATCGCGGCCCGTCGCTGTTTCATCAACGACACCA
 AGGCTTTGGTGCATACCGTAGACGGGACCGCCATGCTGGTCACGCCAGGAATTTCAAGCGCTATGTCCAAGAGCATCCG
 GTGCTTGAAAACTGGCCCAAGCCAAGGAGACGACCGGCTGGAAGCTGGTGCAGCGCGCTTCGAAAAACAGGGGCTTCA
 TCGGAAGACCAGTAAAACTGAACATCTGGACCATCAAGGTTTCTGGTCCTCGCAAGACGAAAGAGCTCAAGGCCTACC
 TGCTCCAGGATCCCAAATTGCTGTTCCCTGAGCAGCCTCTGGACAACCAAGCCTCACGGTCATCACCGATGCCGAAGGA
 GGTGTGGAATGA

Fig. 6B

33A9--ORF2 SEQ ID NO:190

ATGTTTCAACTCCTTTCTGGATATCCAGGAAGCCGTCCCCACCCCAACAACCAAAGCTGCCCCAGGGGGATTATCCT
TCCTCTGAGCAGCATGGAAGTCTCGGCACGCCTCGCCGCGGCAGCTACTGGAGAACATCTGGCAGCGCGCTCGCTAT
CCAAGCAGCAATTCGAGGAGATCTACCGCGGCCACTGGCCAACATATGCCGAGCTGGTCCAGCAGCTCCCTGCTTCGGAA
AATCATCACCATGCCCATCCAGGCGGGATGATCGATCAGGCCTGGAGATCGTGGCCTACGCACTCAAGGTACGGCAGAC
CTACCTGCTCCCGATCGGCGCAGCGCGGAGTCACAGTCAGCCCAGGCTGAAGCCTGGTCCGCCGCGCGGCGTATGGCG
CCCTGGCTCATGACATAGGCAAGATCGTCGTGACCTGCAGGTTGAGCTACAGGACGGCAGCACCTGGCACCCCTTGGAA
GGACCGATCAACCAGCCATACCGCTTCAAGTACGTGAAGTCCCGCGAATACCAGCTCCACGGCGCTGCCTCAGCACTTCT
CATCCACCAACTGCTACCGCGCACTGCACTCGATTGGCTCAGTCGCTTCCAGAGCTGTGGGCTCAATTGATCTACCTGT
TCGCTGGGCAGTACGAGCAGCGCGGGATCCTCGGCGAGATCATCGTGAAGGCAGACCAGGCCTCAGTTGCACAGGAGCTA
GGAGGCAATCCGGATCGAGCTCTGGCTGCACCGAAGCAGTCGCTGCAGCGGCAGTTGGCAGACGGCCTTCGCTTCTTGGT
GAAGGACAAGTTCAAGTTGAATCAACCTAGCGGCCGTCTGATGGATGGCTGACCCAGGACGCACTCTGGCTGGTGAGCA
AGCCTGCTGCCGATCAACTGAGAGCCTACCTGCTGGCCAGGGTATCGATGGGGTGCCCTCCTCTAACCGCGCCGTTCTTC
AGCATGCTCCAGGACCAAGCCGTATCCAGACAAATGCCAGGACAAGGCCATTTGGACGGCCACGGTAGACAACGGTGC
TGGATGGAGAAACAAGTTCACGCTACTCAAGATTGCTCCAGCCTTGATCTGGACAGATGCTGCCGAGCGCCCTCACCCCT
ACAGCGGATCACTGGTCGTTGAAGATGGAACCGCCTCAACGGAAAAGCCGGAACGACCTGTGAAATCCCAACGGGCCG
GCTGAACAGCAGCAAGCACCAGAAACGAAGATGATGCTCCATCAACCTGCGCCGAGCGTTGCGAAACCGGCAACGAGAC
GCAGGCGATTGCGAAACCTCAACTGATGATCAAGAAGAAACAGACGATTTGTATGCACTTCTTGGTAATATCAATTTCG
CACTAGAAGAGCTAGACACTAGCCACGACTCGCCGGCTGCCTCTCCTACGAACACACGCGGGGAGGAGAACCTACAGCAG
CCACTAGGGACCAAGGAGCCAACAGATTGCGCTCCTGAAGCAATTGAAGATGTATTTATGCCTAGCAGAAGTACTGATCT
GGGACAGGGATTCTGTTGGTTGGATGAAATCTGGCATCGCGGCCGTCGCTGTTTCATCAACGACACCAAGGCTTTGGTGC
ATACCGTAGACGGGACCGCCATGCTGGTCACGCCAGGAATTTTCAAGCGCTATGTCCAAGAGCATCCGGTGCTTGAAAA
CTGGCCCAAGCCAAGGAGACGACCGGCTGGAAGCTGGTGCAGCGCGCTTCGAAAAACAGGGGCTTCATCGGAAGACCAG
TAAAAACCTGAACATCTGGACCATCAAGGTTTCTGGTCCTCGCAAGACGAAAGAGCTCAAGGCCTACCTGCTCCAGGATC
CCAAATTGCTGTTCCCTGAGCAGCCTCTGGACAACCCAAGCCTCACGGTCATCACCGATGCCGAAGGAGGTGTGGAATGA

Fig. 6C

ORF 3— 33A9 SEQ ID NO:191

ATGGAAGTCTCGGCACGCCTCGCCGCCGGCAGCTACTGGAGAACATCTGGCAGCGCGCCTCGCTATCCAAGCAGCAATT
 CGAGGAGATCTACCGGCGGCCACTGGCCAACTATGCCGAGCTGGTCCAGCAGCTCCCTGCTTCGGAAAAATCATCACCATG
 CCCATCCAGGCGGGATGATCGATCACGGCCTGGAGATCGTGGCCTACGCACTCAAGGTACGGCAGACCTACCTGCTCCCG
 ATCGGCGCAGCGCCGGAGTCACAGTCAGCCCAGGCTGAAGCCTGGTCCGCCGCCGCGGCGTATGGCGCCCTGGCTCATGA
 CATAGGCAAGATCGTCGTCGACCTGCAGGTTGAGCTACAGGACGGCAGCACCTGGCACCCCTTGGAAACGGACCGATCAACC
 AGCCATACCGCTTCAAGTACGTGAAGTCCCGCGAATACCAGCTCCACGGCGCTGCCTCAGCACTTCTCATCCACCAACTG
 CTACCGCGCACTGCACTCGATTGGCTCAGTCGCTTTCCAGAGCTGTGGGCTCAATTGATCTACCTGTTGCTGGGCAGTA
 CGAGCACGCCGGGATCCTCGGCGAGATCATCGTGAAGGCAGACCAGGCCTCAGTTGCACAGGAGCTAGGAGGCAATCCGG
 ATCGAGCTCTGGCTGCACCGAAGCAGTCGCTGCAGCGGCAGTTGGCAGACGGCCTTCGCTTCTTGGTGAAGGACAAGTTC
 AAGTTGAATCAACCTAGCGGCCCCGTCTGATGGATGGCTGACCCAGGACGCACTCTGGCTGGTGAGCAAGCCTGCTGCCGA
 TCAACTGAGAGCCTACCTGCTGGCCCAGGGTATCGATGGGGTGCCCTCCTCTAACGCGCCGTTCTTCAGCATGCTCCAGG
 ACCAAGCCGTCATCCAGACAAATGCCGAGGACAAGGCCATTTGGACGGCCACGGTAGACAACGGTGCTGGATGGAGAAAC
 AAGTTCACGCTACTCAAGATTGCTCCAGCCTTGATCTGGACAGATGCTGCCGAGCGCCCCCTACCCCTACAGCGGATCACT
 GGTCGTTGAAGATGGAACCGCCTCAACGGAAAAGCCGGAAACGACCTGTGAAATTCCTAACGGGCGGGCTGAACAGCAGC
 AAGCACCAGAAACGAAGATGATGCTCCATCAACCTGCGCCGAGCGTTGCGAAACCGGCAAACGAGACGCAGGCGATTGCG
 AAACCTCAACTGATGATCAAGAAGAAACAGACGATTTGTATGCACTTCTTGGTAATATCAATTGCGCACTAGAAGAGCT
 AGACACTAGCCACGACTCGCCGGCTGCCTCTCTACGAACACACGCGGGGAGGAGAACCTACAGCAGCCACTAGGGACCA
 AGGAGCCAAACAGATTGCGCTCCTGAAGCAATTGAAGATGTATTTATGCCTAGCAGAAGTACTGATCTGGGACAGGGATTCT
 GTTGGTTGGATGAAATCTGGCATCGCGGCCCGTCGCTGTTTATCAACGACACCAAGGCTTTGGTGCATACCGTAGACGG
 GACCGCCATGCTGGTCACGCCAGGAATTTTCAAGCGCTATGTCCAAGAGCATCCGGTGCTTGAAAACTGGCCCAAGCCA
 AGGAGACGACCGGCTGGAAGCTGGTGCAGCGCGCTTCGAAAAACAGGGGCTTCATCGGAAGACCAGTAAAAACCTGAAC
 ATCTGGACCATCAAGGTTTCTGGTCCTCGCAAGACGAAAGAGCTCAAGGCCTACCTGCTCCAGGATCCCAAATTGCTGTT
 CCCTGAGCAGCCTCTGGACAACCCAAGCCTCACGGTCATCACCGATGCCGAAGGAGGTGTGGAATGA

Fig. 6D

ORF 4--33A9 SEQ ID NO:192

ATGATCGATCACGGCCTGGAGATCGTGGCCTACGCACTCAAGGTACGGCAGACCTACCTGCTCCCGATCGGCGCAGCGCC
 GGAGTCACAGTCAGCCCAGGCTGAAGCCTGGTCGGCCGCCGCGCGGTATGGCGCCCTGGCTCATGACATAGGCAAGATCG
 TCGTCGACCTGCAGGTTGAGCTACAGGACGGCAGCACCTGGCACCCCTTGAACGGACCGATCAACCAGCCATACCGCTTC
 AAGTACGTGAAGTCCCGCGAATACCAGCTCCACGGCGCTGCCTCAGCACTTCTCATCCACCAACTGCTACCGCGCACTGC
 ACTCGATTGGCTCAGTCGCTTTCAGAGCTGTGGGCTCAATTGATCTACCTGTTGCTGGGAGTACGAGCAGCCGGGA
 TCCTCGGCAGATCATCGTGAAGGCAGACCAGGCCTCAGTTGCACAGGAGCTAGGAGGCAATCCGGATCGAGCTCTGGCT
 GCACCGAAGCAGTCGCTGCAGCGGCAGTTGGCAGACGGCCTTCGCTTCTTGGTGAAGGACAAGTTCAAGTTGAATCAACC
 TAGCGGCCCGTCTGATGGATGGCTGACCCAGGACGCACTCTGGCTGGTGAAGCCTGCTGCCGATCAACTGAGAGCCT
 ACCTGCTGGCCCAGGGTATCGATGGGGTGCCCTCCTCTAACGCGCCGTTCTTCAGCATGCTCCAGGACCAAGCCGTCATC
 CAGACAAATGCCGAGGACAAGGCCATTTGGACGGCCACGGTAGACAACGGTGCTGGATGGAGAAAACAGTTACGCTACT
 CAAGATTGCTCCAGCCTTGATCTGGACAGATGCTGCCGAGCGCCCTCACCTACAGCGGATCACTGGTCGTTGAAGATG
 GAACCGCCTCAACGGAAAAGCCGGAACGACCTGTGAAATTCCTAACGGGCCGGCTGAACAGCAGCAAGCACCAGAAACG
 AAGATGATGCTCCATCAACCTGCGCCGAGCGTTGCGAAAACGGCAAACGAGACGAGGCGATTGCGAAAACCTCAACTGA
 TGATCAAGAAGAAAACAGACGATTTGTATGCACTTCTTGGTAATATCAATTGCCACTAGAAGAGCTAGACACTAGCCACG
 ACTCGCCGGCTGCCTCTCTACGAACACACGCGGGGAGGAGAACCTACAGCAGCCACTAGGGACCAAGGAGCCAACAGAT
 TGGCTCCTGAAGCAATTGAAGATGTATTTATGCCTAGCAGAAGTACTGATCTGGGACAGGGATTGTTGGTTGGATGAA
 ATCTGGCATCGCGCCCGTGCCTGTTTCATCAACGACACCAAGGCTTTGGTGCATACCGTAGACGGGACCGCCATGCTGG
 TCACGCCAGGAATTTTCAAGCGCTATGTCCAAGAGCATCCGGTGCTTGAAAACTGGCCCAAGCCAAGGAGACGACCGGC
 TGAAGCTGGTGCAGCGCGCTTCGAAAAACAGGGGCTTCATCGGAAGACCAGTAAAACTGAACATCTGGACCATCAA
 GGTTCCTGGTCTCGCAAGACGAAAGAGCTCAAGGCCTACCTGCTCCAGGATCCCAAATTGCTGTTCCCTGAGCAGCCTC
 TGGACAACCCAAGCCTCACGGTCATACCGATGCCGAAGGAGGTGTGGAATGA

Fig. 6E

ORF5--33A9 SEQ ID NO:193

ATGCTCCAGGACCAAGCCGTCATCCAGACAAATGCCGAGGACAAGGCCATTTGGACGGCCACGGTAGACAACGGTGCTGG
 ATGGAGAAACAAGTTCACGCTACTCAAGATTGCTCCAGCCTTGATCTGGACAGATGCTGCCGAGCGCCCTCACCTACA
 GCGGATCACTGGTCGTTGAAGATGGAACCGCCTCAACGGAAAAGCCGGAACGACCTGTGAAATTCCCAACGGGCCGGCT
 GAACAGCAGCAAGCACCAGAAACGAAGATGATGCTCCATCAACCTGCGCCGAGCGTTGCGAAACCGGCAACGAGACGCA
 GCGGATTGCGAAACCTCAACTGATGATCAAGAAGAAACAGACGATTTGTATGCACTTCTTGGTAATATCAATTCGCCAC
 TAGAAGAGCTAGACACTAGCCACGACTCGCCGGCTGCCTCTCTACGAACACACGCGGGGAGGAGAACCCTACAGCAGCCA
 CTAGGGACCAAGGAGCCAACAGATTGCGCTCCTGAAGCAATTGAAGATGTATTTATGCCTAGCAGAAGTACTGATCTGGG
 ACAGGGATTGTTGGTTGGATGAAATCTGGCATCGCGGCCCGTGCCTGTTTCATCAACGACACCAAGGCTTTGGTGCATA
 CCGTAGACGGGACCGCCATGCTGGTCACGCCAGGAATTTTCAAGCGCTATGTCCAAGAGCATCCGGTGCTTGAAAACTG
 GCCCAAGCCAAGGAGACGACCGGCTGGAAGCTGGTGCAGCGCGCTTCGAAAAACAGGGGCTTCATCGGAAGACCAGTAA
 AACCTGAACATCTGGACCATCAAGTTTCTGGTCTCGCAAGACGAAAGAGCTCAAGGCCTACCTGCTCCAGGATCCCA
 AATTGCTGTTCCCTGAGCAGCCTCTGGACAACCCAAGCCTCACGGTCATACCGATGCCGAAGGAGGTGTGGAATGA

Fig. 6F

ORF6--33A9 SEQ ID NO:194

ATGATGCTCCATCAACCTGCGCCGAGCGTTGCGAAACCGGCAAACGAGACGCAGGCGATTGCGAAACCCTCAACTGATGA
TCAAGAAGAAACAGACGATTTGTATGCACTTCTTGGTAATATCAATTCGCCACTAGAAGAGCTAGACACTAGCCACGACT
CGCCGGCTGCCTCTCCTACGAACACACGCGGGGAGGAGAACCCTACAGCAGCCACTAGGGACCAAGGAGCCAACAGATTGC
GCTCCTGAAGCAATTGAAGATGTATTTATGCCTAGCAGAAGTACTGATCTGGGACAGGGATTTCGTTGGTTGGATGAAATC
TGGCATCGCGGCCCGTCGCCTGTTTCATCAACGACACCAAGGCTTTGGTGCATACCGTAGACGGGACCGCCATGCTGGTCA
CGCCAGGAATTTTCAAGCGCTATGTCCAAGAGCATCCGGTGCTTGAAAACTGGCCCAAGCCAAGGAGACGACCGGCTGG
AAGCTGGTGCAGCGCGCTTCGAAAAACAGGGGCTTCATCGGAAGACCAGTAAAAACCTGAACATCTGGACCATCAAGGT
TTCTGGTCTCGCAAGACGAAAGAGCTCAAGGCCTACCTGCTCCAGGATCCCAAATTGCTGTTCCCTGAGCAGCCTCTGG
ACAACCAAGCCTCACGGTCATCACCGATGCCGAAGGAGGTGTGGAATGA

Fig. 6G

ORF7--33A9 SEQ ID NO:195

ATGCTCCATCAACCTGCGCCGAGCGTTGCGAAACCGGCAAACGAGACGCAGGCGATTGCGAAACCCTCAACTGATGATCA
AGAAGAAACAGACGATTTGTATGCACTTCTTGGTAATATCAATTCGCCACTAGAAGAGCTAGACACTAGCCACGACTCGC
CGGCTGCCTCTCCTACGAACACACGCGGGGAGGAGAACCCTACAGCAGCCACTAGGGACCAAGGAGCCAACAGATTGCGCT
CCTGAAGCAATTGAAGATGTATTTATGCCTAGCAGAAGTACTGATCTGGGACAGGGATTTCGTTGGTTGGATGAAATCTGG
CATCGCGGCCCGTCGCCTGTTTCATCAACGACACCAAGGCTTTGGTGCATACCGTAGACGGGACCGCCATGCTGGTCACGC
CAGGAATTTTCAAGCGCTATGTCCAAGAGCATCCGGTGCTTGAAAACTGGCCCAAGCCAAGGAGACGACCGGCTGGAAG
CTGGTGCAGCGCGCTTCGAAAAACAGGGGCTTCATCGGAAGACCAGTAAAAACCTGAACATCTGGACCATCAAGGTTTC
TGGTCTCGCAAGACGAAAGAGCTCAAGGCCTACCTGCTCCAGGATCCCAAATTGCTGTTCCCTGAGCAGCCTCTGGACA
ACCAAGCCTCACGGTCATCACCGATGCCGAAGGAGGTGTGGAATGA

Fig. 6H

ORF8--33A9 SEQ ID NO:196

ATGCCTAGCAGAAGTACTGATCTGGGACAGGGATTTCGTTGGTTGGATGAAATCTGGCATCGCGGCCCGTCGCCTGTTTCAT
CAACGACACCAAGGCTTTGGTGCATACCGTAGACGGGACCGCCATGCTGGTCACGCCAGGAATTTTCAAGCGCTATGTCC
AAGAGCATCCGGTGCTTGAAAACTGGCCCAAGCCAAGGAGACGACCGGCTGGAAGCTGGTGCAGCGCGCTTCGAAAAA
CAGGGGCTTCATCGGAAGACCAGTAAAAACCTGAACATCTGGACCATCAAGGTTTCGTTGGTCTCGCAAGACGAAAGAGCT
CAAGGCCTACCTGCTCCAGGATCCCAAATTGCTGTTCCCTGAGCAGCCTCTGGACAACCAAGCCTCACGGTCATCACCG
ATGCCGAAGGAGGTGTGGAATGA

Fig. 6I

ORF9--33A9 SEQ ID NO:197

ATGAAATCTGGCATCGCGGCCCGTCGCCTGTTTCATCAACGACACCAAGGCTTTGGTGCATACCGTAGACGGGACCGCCAT
GCTGGTCACGCCAGGAATTTTCAAGCGCTATGTCCAAGAGCATCCGGTGCTTGAAAACTGGCCCAAGCCAAGGAGACGA
CCGGCTGGAAGCTGGTGCAGCGCGCTTCGAAAAACAGGGGCTTCATCGGAAGACCAGTAAAAACCTGAACATCTGGACC
ATCAAGGTTTCTGGTCTCGCAAGACGAAAGAGCTCAAGGCCTACCTGCTCCAGGATCCCAAATTGCTGTTCCCTGAGCA
GCCTCTGGACAACCAAGCCTCACGGTCATCACCGATGCCGAAGGAGGTGTGGAATGA

Fig. 6J

ORF10-33A9 SEQ ID NO:198

ATGCTGGTCACGCCAGGAATTTTCAAGCGCTATGTCCAAGAGCATCCGGTGCTTGAAAACTGGCCCAAGCCAAGGAGAC
GACCGGCTGGAAGCTGGTGCAGCGCGCTTCGAAAAACAGGGGCTTCATCGGAAGACCAGTAAAAACCTGAACATCTGGA
CCATCAAGGTTTCTGGTCTCGCAAGACGAAAGAGCTCAAGGCCTACCTGCTCCAGGATCCCAAATTGCTGTTCCCTGAGCA
CAGCCTCTGGACAACCAAGCCTCACGGTCATCACCGATGCCGAAGGAGGTGTGGAATGA

Fig. 6K

ORF 1--33A9 SEQ ID NO:199

MEPPMFQLLSWISRKPSPTPTTKAAPGGFILPLSSMELLGTPRRRQLENIWQRASLSKQQFEEIYRRPLANYAELVQQL
PASENHHHAHPGGMIDHGLEIVAYALKVRQTYLLPIGAAPESQSAQAEAWSAAAAAYGALAHDIGKIVVDLQVELQDGSTW
HPWNGPINQPYRFKYVKSREYQLHGAASALLIHQLLPRTALDWLSRFPELWAQLIYLFAGQYEHAGILGEIIVKADQASV
AQELGGNPDRAAAPKQSLQRLADGLRFLVKDKFKLNQPSGPGSDGWLTQDALWLVSKEPAADQLRAYLLAQGIDGVPSSN
APFFSMLQDQAVIQTNAEDKAIWTATVDNGAGWRNKFTLLKIAPALIWTDAERPSPYSGSLVVEDGTASTEKPETTC
PNGPAEQQAPETKMLHQPAPSVAKPANETQAIAPSTDDQETDDLYALLGNINSPLEELDTSHDSPAASPTNTRGEE
NLQQLPLGTKEPTDCAPEAIEDVFMPSTRSTDLGQGFVGMKSGIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEH
VLEKLAQAKETTGWKLVRQAFKQGLHRKTSKNLNIWTIKVSGPRKTKELKAYLLQDPKLLFPEQPLDNPSLTIVITDAEG
GVE.

Fig. 6L

ORF2--33A9 SEQ ID NO:200

MFQLLSWISRKPSPTPTTKAAPGGFILPLSSMELLGTPRRRQLENIWQRASLSKQQFEEIYRRPLANYAELVQQLPASE
NHHHAHPGGMIDHGLEIVAYALKVRQTYLLPIGAAPESQSAQAEAWSAAAAAYGALAHDIGKIVVDLQVELQDGSTWHPWN
GPINQPYRFKYVKSREYQLHGAASALLIHQLLPRTALDWLSRFPELWAQLIYLFAGQYEHAGILGEIIVKADQASVAQEL
GGNPDRAAAPKQSLQRLADGLRFLVKDKFKLNQPSGPGSDGWLTQDALWLVSKEPAADQLRAYLLAQGIDGVPSSNAPFF
SMLQDQAVIQTNAEDKAIWTATVDNGAGWRNKFTLLKIAPALIWTDAERPSPYSGSLVVEDGTASTEKPETTC
AEQQQAPETKMLHQPAPSVAKPANETQAIAPSTDDQETDDLYALLGNINSPLEELDTSHDSPAASPTNTRGEENLQ
PLGTKEPTDCAPEAIEDVFMPSTRSTDLGQGFVGMKSGIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEHVLEK
LAQAKETTGWKLVRQAFKQGLHRKTSKNLNIWTIKVSGPRKTKELKAYLLQDPKLLFPEQPLDNPSLTIVITDAEGGVE.

Fig. 6M

ORF2-33A9 SEQ ID NO:201

MELLGTPRRRQLENIWQRASLSKQQFEEIYRRPLANYAELVQQLPASENHHHAHPGGMIDHGLEIVAYALKVRQTYLLP
 IGAAPESSQSAQAEAWSAAAAYGALAHDIGKIVVDLQVELQDGSTWHPWNGPINQPYRFKYVKSREYQLHGAASALLIHQL
 LPRTALDWLSRFPPELWAQLIYLFAGQYEHAGILGEIIVKADQASVAQELGGNPDRAAPKQSLQRQLADGLRFLVKDKF
 KLNQPSGSPSDGWLTDALWLVSKPAADQLRAYLLAQGIDGVPSSNAPFFSMLQDQAVIQTNAEDKAIWTATVDNGAGWRN
 KFTLLKIAPALIWTDAERPSPYSGSLVVEDGTASTEKPETTCEIPNGPAEQQAPETKMMLHQPAPSVAKPANETQAI
 KPSTDDQEETDDLYALLGNINSPLEELDTSHDSPAASPTNTRGEENLQQPLGTKEPTDCAPEAIEDVFMPSSRSTDLGQGF
 VGWMKSGIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEHVPLEKLAQAKETTGWKLQVQRAFEKQGLHRKTSKNLN
 IWTIKVSGPRKTKELKAYLLQDPKLLFPEQPLDNPSLTVITDAEGGVE.

Fig. 6N

ORF4-33A9 SEQ ID NO:202

MIDHGLEIVAYALKVRQTYLLPIGAAPESQSAQAEAWSAAAAYGALAHDIGKIVVDLQVELQDGSTWHPWNGPINQPYRF
 KYVKSREYQLHGAASALLIHQLLPRTALDWLSRFPPELWAQLIYLFAGQYEHAGILGEIIVKADQASVAQELGGNPDRA
 APKQSLQRQLADGLRFLVKDKFKLNQPSGSPSDGWLTDALWLVSKPAADQLRAYLLAQGIDGVPSSNAPFFSMLQDQAVI
 QTNAEDKAIWTATVDNGAGWRNKFTLLKIAPALIWTDAERPSPYSGSLVVEDGTASTEKPETTCEIPNGPAEQQAPET
 KMMLHQPAPSVAKPANETQAIKPSTDDQEETDDLYALLGNINSPLEELDTSHDSPAASPTNTRGEENLQQPLGTKEPTD
 CAPEAIEDVFMPSSRSTDLGQGFVGWMKSGIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEHVPLEKLAQAKETT
 GWKLQVQRAFEKQGLHRKTSKNLN IWTIKVSGPRKTKELKAYLLQDPKLLFPEQPLDNPSLTVITDAEGGVE.

Fig. 6O

ORF5--33A9 SEQ ID NO:203

MLQDQAVIQTNAEDKAIWTATVDNGAGWRNKFTLLKIAPALIWTDAERPSPYSGSLVVEDGTASTEKPETTCEIPNGPA
 EQQAPETKMMLHQPAPSVAKPANETQAIKPSTDDQEETDDLYALLGNINSPLEELDTSHDSPAASPTNTRGEENLQQP
 LGTKEPTDCAPEAIEDVFMPSSRSTDLGQGFVGWMKSGIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEHVPLEK
 LAQAKETTGWKLQVQRAFEKQGLHRKTSKNLN IWTIKVSGPRKTKELKAYLLQDPKLLFPEQPLDNPSLTVITDAEGGVE.

Fig. 6P

MMLHQPAAPSVAKPANETQAIAKPSTDDQEETDDLYALLGNINSPLEELDTSHDSPAASPTNTRGEENLQOPLGTKEPTDC
 APEAIEDVFMPSRSTDLGGFGVGMKSGIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEHVPVLEKLAQAKETTGW
 KLVQRAFEKQGLHRKTSKNLNIWTIKVSGPRKTKELKAYLLQDPKLLFPEQPLDNPPLSLTVITDAEGGVE.

ORF7-33A9 SEQ ID NO:205

MLHQPA PSVAKPANETQAI AKPSTDDQEETDDLYALLGNINSPLEELDTSHDSPAASPTNTRGEENLQQPLGTKEPTDCA
PEAIEDVFMPSRSTDLGQGFGVWMSGIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEHVPLEKLAQAKETTGWK
LVORAFEKOGHLHRKTSKNLNIWTIKVS GPRKTKELKAYLLODPKLLFPEOPLDNPSLTVITDAEGGVE.

ORF8--33A9 SEQ ID NO:206

MPSRSTDLGQGFVGMKSGIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEHVPLEKLAQAKETTGWRLVQRAFEK
OGLHRKTSKNLNIWTIKVSGPRKTKELKAYLLQDPKLLFPEOPLDNPSLTVITDAEGGVE.

ORF9--33A9 SEQ ID NO:207

MKSGIAARRLFINDTKALVHTVDGTAMLVTPGIFKRYVQEHVPLEKLAQAKETTGWKLVQRAFEKQGLHRKTSKNLNIWT
 IKVSGPRKTKELKAYLLODPKLLFPEOPLDNPSLTVITDAEGGVE.

Fig. 6T

ORF10--33A9 SEQ ID NO:208

MLVTPGIFKRYVQEHVPLEKLAQAKETTGWKLVRFAFEKQGLHRKTSKNLNIWTIKVSGPRKTKELKAYLLQDPKLLFPE
QPLDNPSLTVITDAEGGVE.

Fig. 6U

34B12 EcoRI fragment Map (1 > 4590) ORF Map

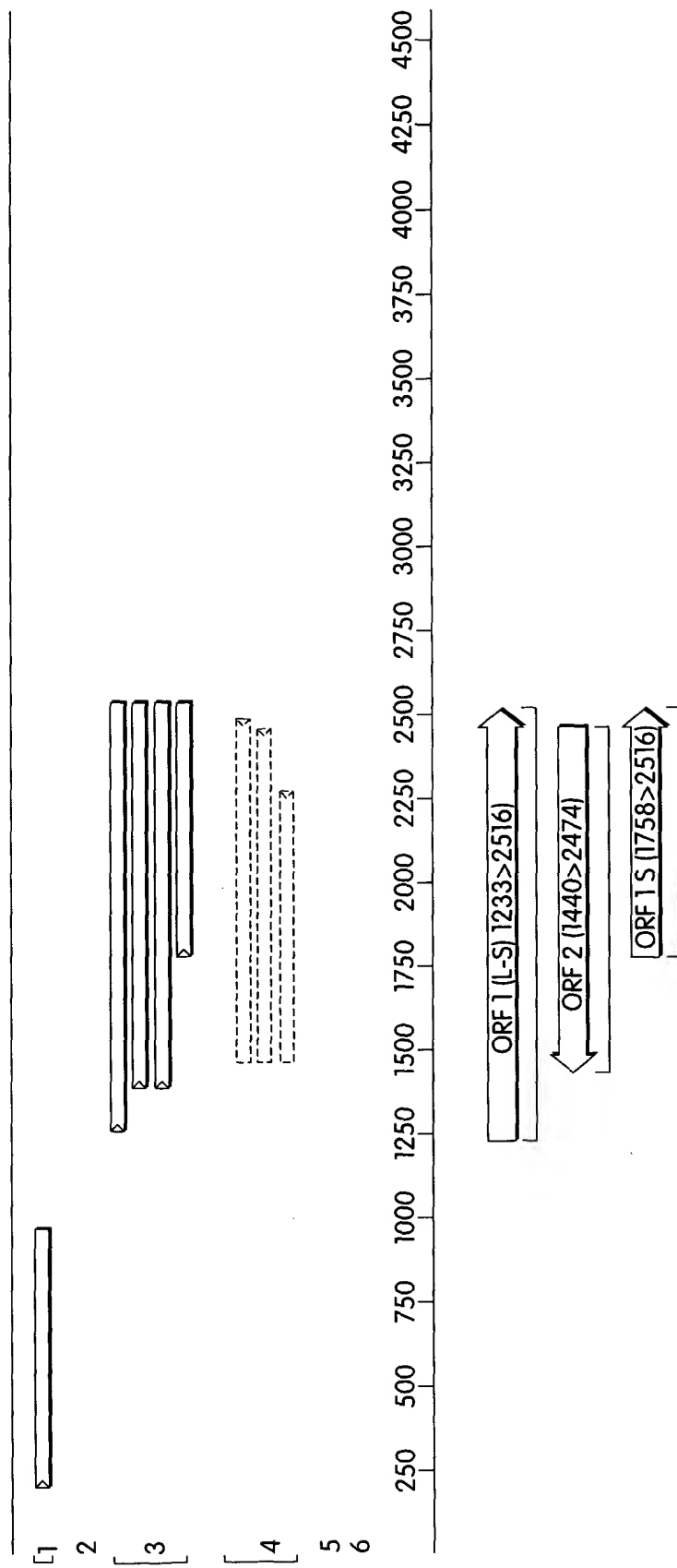


Fig. 7A

Sequence: 34B12 EcoRI fragment From: 1 To: 4590

10	20	30	40	50	60
GAATTCCATG	GCGCCGTGGA	GGAGGCTTCC	GAGTCGCCCG	TGGCAGGCGT	ACGGGCCCGC 60
AACTACCAGG	TCGACCTGGA	CGATGCGAGC	TTTGCCCGCC	AGGTAGAACG	CCTGCAGGCC 120
CACGTGAGGG	CCGGCGACGT	GTTCCAGATC	GTACCTTCGC	GCAGCTTCAG	CATGCCGTGC 180
GCGGACCCCT	GGCGGGCCTA	TCGCCAGTTG	TGCCTGCGCA	ACCCAGCC	GTACCGCTTC 240
TTCTTCGATG	CGGGGACTT	CTGCCTGTTT	GGCGCTTCGC	CGGAGTCGGC	ATTGAAGTAC 300
310	320	330	340	350	360
GACGCGGAGA	GTCGCGAGGT	GGAACCTCTAT	CCCATTGCCG	GCACCCGCCC	GCGCGGATGC 360
GATGCCCCGG	GCGCCATCGA	TGCGGAAGTG	GACAATCGCC	TGGAAGCGGA	GTTGCGCCTG 420
GATGCCAAGG	AGATCGCCGA	GCACATGATG	CTGGTCGACC	TGGCGCGCAA	CGATCTGGCG 480
CGCGTCTGCC	GCAGCGGTAC	CCGGCAGGTG	CGCGACATGC	TCAAGGTCGA	TCGCTACAGC 540
CACGTGATGC	ACCTGGTCTC	GCGCGTGGCT	GGCGAAGTGC	ACGGCGAACT	GGATGCGCTG 600
610	620	630	640	650	660
CATGCCTACC	GTGCCTGCCT	GAACATGGGC	ACCCTGGTCG	GCGCGCCGAA	GGTCCGTGCC 660
ATGCAGTTGC	TGCGGCAGTA	CGAGGATGGC	TATCGCGGCA	GCTACGGTGG	TGCGATCGGC 720
ATTCTCGACA	GCGCCGGCAA	CCTCGATACC	AGCATTGTCA	TCCGCTCCGC	CGAGGTCCGC 780
GAAGGTATCG	CGCGGGTTCG	GGCAGGCGCC	GGCGTGGTGC	TGGATTCCGA	TCCACGGCTG 840
GAGGCCGAGG	AAACCCGCAA	CAAGGCGCTG	GCGGTGCTGA	CCGCCGTGGC	CGCTGCCGAA 900
910	920	930	940	950	960
CGCGAAAGGG	GAGAGCGCGA	TGCGCATCAC	GCTGTTGGAT	AACTTCGATT	CCTTCACCTA 960
CAACCTGGTC	GAGCAGTTCT	GCCTGCTCGG	CGCGGAGGTC	CGGGTGATGC	GCAACGATAC 1020
GCCGTTGCCG	ACGATCCAGG	CGGCATTGCT	GGCCGACGGT	TGCGAACTGC	TGGTGCTGTC 1080
GCCGGGGCCC	GGTCGGCCGG	AAGACGCCGG	CTGTATGCTG	GAATTGCTCG	CCTGGGCCCCG 1140
CGGGCGCTTG	CCGGTGCTCG	GCGTCTGCCT	CGGCCACCAG	GCGCTGGCGC	TGGCCGCCGG 1200
1210	1220	1230	1240	1250	1260
TGGCGCGGTG	GGCGAGGCGA	GGAAGCCGCT	GCATGGCAAG	AGCACGTCCC	TGCGTTTCGA 1260
TCAGCGTCAC	CCGCTGTTCG	ACGGCATCGC	TGACCTGCGC	GTCGCGCGCT	ACCACTCGCT 1320
GGTGGTCAGT	CGCCTGCCGG	AAGGTTTCGA	CTGCCTGGCC	GATGCCGATG	GCGAGATCAT 1380
GGCGATGGCC	GATCCGCGCA	ATCGACAGCT	GGGCTTGCAA	TTCCATCCCG	AGTCGATTCT 1440
CACCACCCAC	GGCCAGCGTC	TGCTGGAGAA	CGCTCTACTC	TGGTGCGGCG	CGTTGGCGGT 1500

Fig. 7B

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Sequence: 34B12 EcoRI fragment From: 1 To: 4590

1510						1520						1530						1540						1550						1560					
CGCGGAGCGC CTTCGGGCCT GAGCGGCGCT GCGCAGTTTC GACCGAGGCT CGGTTGCCAG 1560																																			
GCCGGCGCAT CGTCGAAACG CTGGCGGCC AGTTCGCGCA GGCGCTGGCG GGCGCTTTCG 1620																																			
AGAAAGCGAC GGAAGCTGCG CTCGGATTCC AGCGCGGTGT TGTAAGTAGCA ATACACCTTG 1680																																			
GTGTCGATGC CGCCCGGTTT GTACAGTTCG CTGAGGACTG CCAGGGTACC GTTGCGCAGG 1740																																			
CGTTCCTCGA CGAAATAATG CGGCGAGATG CCCCATCCGA CGCCGGCTTC CACCAGACGC 1800																																			
1810						1820						1830						1840						1850						1860					
AGCATGTCGT CGAAGTTTTT CACGAAGAGC ACCTTGTCGC TGACCGGCCG CAGCAGGTTT 1860																																			
GAATGCTGCC CGGAGCGGCT GCCGAGGCTG ATCTGCCGGT AATTGGCCAG GCTCGCGATG 1920																																			
CTGTGCAGGG AGGCATTGCA CAACGGGTGC TGGCGATGGG CGACGACGAA CGCCTTGGTG 1980																																			
TAGCCGAGCA CGCACTGGTT GAAGCGGGAG ATCTTCAGTT CCTCGTCGAT GGTGATGGCG 2040																																			
ATATCGATTT CCGCGTTGTC CTGCTTGATC GTCGCCAGGC TATCGGCGGG CGAGGTGCGT 2100																																			
2110						2120						2130						2140						2150						2160					
ATCAGGCTGA CCATGTTGAA ATCGTCGAGC AGTACGCTGC TCACCGTATC GCAGAACGAC 2160																																			
GGCGGGATGG CCGTGTCCAG CAGCACCCGG AGATTGCGCG GACCCTTGTT GAGATTGAAG 2220																																			
GCGATGTCGC CGATCAGCTG CTGGTAGTTC AGCAGGCTGC GCATGTAAGG GATCAGGCGA 2280																																			
AGCGCCTGCT CCGTGGGTTT GACCTTGTA CCGTCCCGAC GGACCAGCTC CACGCACAGG 2340																																			
TCGATTTCCA GGTTGCTGAC CGCCGAGCTG ACCGCGGTGT GCGACTTGCG CAGGATCCGC 2400																																			
2410						2420						2430						2440						2450						2460					
GCAGCGGAGG AAATCGAACC GGAGGCGATG ACCTGGAGGA ACATGTTTAC GTGATTCAGG 2460																																			
TTATGAATAG GCATCCCTTA TTCCTTTTAT TGGGTGGCGC GTGCCGCTTC CCTTGATCGG 2520																																			
GTCAGGTTGC CGCTACTGTG GAAGAAGCGT CGAGGACTCG ATAGATAGCG CCCGAGTGTT 2580																																			
TCAACTTGTC TTCTGGATGA CGTTTTTCATC GGGGAAACCT CCCGTCGGTC AGTGAATCGC 2640																																			
AAGGGCTGGC GTGCGAGGGT GGAATCGGCC GCCGGCTCGC TTTCTGCGCG GCGGGCGCAC 2700																																			
2710						2720						2730						2740						2750						2760					
GGCACGGGGA GTCGTCGTTT TGGAGGTGAG GGATGACGGC TCTGTTTCAG GATATTTTTA 2760																																			
TAATTATGTG AAAGAAGAGC TTATTTCAAC GAAATATGTT TCATATTGCT CGTTAAATTC 2820																																			
GACGAAAAGA AAATCCGGAT ATTTACCGGT TATTTAACGC TAATACCAAG TGCCTAATAC 2880																																			
CAAAGTATTA ACGCTGGTAT GCCGGCATGT CGTGTTCGGT CGTGGAGCGA GCCGAGCTAG 2940																																			
GGACGGTTCT AATAAACCAA AAAATTATGT CGCGTACGTC TAACGACCGA AACCTATGTC 3000																																			

Fig. 7C

Sequence: 34B12 EcoRI fragment From: 1 To: 4590

3010		3020		3030		3040		3050		3060	
TCTTGTTAGC	GTAGCCACCG	GCCAGGCCGG	TACGGACCCG	GGATGGCCCT	GGCGCGACCT	3060					
ATGCGGTTAG	AATCCGCGGC	CTTGCAAGCG	GATACCCGAG	CTTCGCTCGA	AGGTGTCGCG	3120					
GTGCCGTGCC	GTGGAATCGG	CCGCCGGCTC	GCTTTCTGCG	CGGCGGGCGC	ACGGCGACGG	3180					
GGAGTCGTCG	TTTTTGAGGT	GAGGGATGAC	GGCTCTGTTT	CAGGATATTT	TTATAATTAT	3240					
GTGAAAGAAG	AGCTTATTTT	AACGAAATAT	GTTTCATATT	GCTCGTAAAT	TCGACGAAAA	3300					
3310		3320		3330		3340		3350		3360	
GAAAATCCGG	ATATTTACCG	GTTATTTAAC	GTTAATACCA	AGGGCCTAAT	ACCAAAGTAT	3360					
TAACGCTGGC	ATGCCGGCAT	GTCGTGTTTC	GTCGTGGAGC	GAGCCGAGCC	AGGAACGGTT	3420					
CTAAGAAACG	AAAAAATTAT	GTCGCGTAGG	TCTAACGACC	GAAACCTATG	TCTTTTGTTA	3480					
GCGTAGCCAC	CGGCCAGGCC	GGTACGGATG	CCGGGATGGC	CCTGGCGCGA	CCTATGCGGT	3540					
TAGAATCCGC	GGCCTTGCA	GCGGATCCCC	GGGGTTTGCT	CAAGGGGACA	CGGGTGCCGT	3600					
3610		3620		3630		3640		3650		3660	
GCCCGAAACC	TGCAATCGTC	AGTTCCTGTC	GGTCCAGCCT	GCCGCCGGGT	ATAAAATCGA	3660					
GAGACGCGCT	GTTGCGCCTT	CAGGTGTAGC	GACTATGACG	CACATTTCCG	AACGACTCCT	3720					
GGTACAGGCC	CACCTGGCCG	CCAAGCAACC	CCGTGTGTTG	AGCGAGCAGG	AGAGCGCCGA	3780					
GCATCGCGCG	GCGATCGCGG	CCGAACTGAA	GGCGCAAAAT	GCTGTACTGG	TGGCGCATTG	3840					
CTACTGCGAC	CCGGTGATCC	AGGCGTTGGC	CGAGGAGACC	GGCGGTTGCG	TATCCGATTC	3900					
3910		3920		3930		3940		3950		3960	
GCTGGAGATG	GCCCCTTTTC	GCAACCAGCA	TCCGGCGCAG	ACGGTGGTCG	TGGCCGGGGT	3960					
GCGCTTCATG	GGCGAGACGG	CGAAGATCCT	CAACCCTGAG	AAGCGTGTGC	TGATGCCGAC	4020					
CCTCGAAGCG	ACCTGCTCGC	TCGACCTGGG	ATGCCCGGTG	GATGAATTCT	CGGCTTTCTG	4080					
CGACCAGCAC	CCGGAACGGA	CCGTGGTGGT	CTATGCGAAC	ACCTCCGCGG	CGGTGAAGGC	4140					
ACGCGCCGAC	TGGGTCGTGA	CCTCCAGTTG	CGCGGTGGAG	ATCGTCGAAC	ACCTGATGGA	4200					
4210		4220		4230		4240		4250		4260	
CAACGGCGAG	CCCATCCTCT	GGGCGCCGGA	CCAGCACCTG	GGACGCTACA	TCCAGCGCGA	4260					
GACGGGGGCC	GACATGCTGC	TCTGGGATGG	CGCCTGTATC	GTCCACGAGG	AGTTCAAGGC	4320					
CAAGCAGCTG	GAAGACATGA	AGGCGCTCTA	CCCGGACGCC	GCCATCCTGG	TCCACCCCGA	4380					
ATCGCCGGAA	AGCGTGGTCG	CGCTGGCCGA	TGCCGTGGGC	TCGACCAGCC	AGTTGATCAA	4440					
GGCCGCGCAG	ACCCTGCCGA	ACAAGACCTT	CATCGTCGCC	ACCGATCGCG	GCATCTTCTA	4500					

Fig. 7D

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Sequence: 34B12 EcoR1 fragment From: 1 To: 4590

4510 4520 4530 4540 4550 4560
 CAAGATGCAG CAGTTGTGCC CGGACAAGGA TTTCATCGAG GCCCCACCG CCGGCAACGG 4560
 CGCCGCCTGC CGCAGTGC GC ACTGCCCG 4590

Fig. 7E

[illegible]

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Sequence: 34B12 ORF 1 L-S From: 1 To: 1284

10	20	30	40	50	60
ATGGCAAGAG	CACGTCCCTG	CGTTTCGATC	AGCGTCACCC	GCTGTTTCGAC	GGCATCGCTG 60
ACCTGCGCGT	CGCGCGCTAC	CACTCGCTGG	TGGTCAGTCG	CCTGCCGGAA	GGTTTCGACT 120
GCCTGGCCGA	TGCCGATGGC	GAGATCATGG	CGATGGCCGA	TCCGCGCAAT	CGACAGCTGG 180
GCTTGCAATT	CCATCCCGAG	TCGATTCTCA	CCACCCACGG	CCAGCGTCTG	CTGGAGAACG 240
CTCTACTCTG	GTGCGGCGCG	TTGGCGGTCTG	CGGAGCGCCT	TCGGGCCTGA	GCGGCGCTGC 300
310	320	330	340	350	360
GCAGTTTCGA	CCGAGGCTCG	GTTGCCAGGC	CGGCGCATCG	TCGAAACGCT	GGCGGCCAG 360
TTCGCGCAGG	CGCTGGCGGG	CGCTTTTCGAG	AAAGCGACGG	AAGCTGCGCT	CGGATTCCAG 420
CGCGGTGTTG	TAGTAGCAAT	ACACCTTGGT	GTCGATGCCG	CCCGGTTCTG	ACAGTTCGCT 480
GAGGACTGCC	AGGGTACCGT	TGCGCAGGCG	TTCTTCGACG	AAATAATGCG	GCGAGATGCC 540
CCATCCGACG	CCGGCTTCCA	CCAGACGCAG	CATGTCGTCG	AAGTTTTTCCA	CGAAGAGCAC 600
610	620	630	640	650	660
CTTGTCGCTG	ACCGGCCGCA	GCAGGTTTCGA	ATGCTGCCCCG	GAGCGGCTGC	CGAGGCTGAT 660
CTGCCGGTAA	TTGGCCAGGC	TCGCGATGCT	GTGCAGGGAG	GCATTGCACA	ACGGGTGCTG 720
CGGATGGGCG	ACGACGAACG	CCTTGGTGTA	GCCGAGCACG	CACTGGTTGA	AGCGGGAGAT 780
CTTCAGTTCC	TCGTCGATGG	TGATGGCGAT	ATCGATTTC	GCGTTGTCTT	GCTTGATCGT 840
CGCCAGGCTA	TCGGCGGGCG	AGGTGCGTAT	CAGGCTGACC	ATGTTGAAAT	CGTCGAGCAG 900
910	920	930	940	950	960
TACGCTGCTC	ACCGTATCGC	AGAACGACGG	CGGGATGGCG	GTGTCCAGCA	GCACCCGGAG 960
ATTGCGCGGA	CCCTTGTTGA	GATTGAAGGC	GATGTCGCCG	ATCAGCTGCT	GGTAGTTCAG 1020
CAGGCTGCGC	ATGTAAGGGA	TCAGGCGAAG	CGCCTGCTCG	GTGGGTTCGA	CCTTGTAGCC 1080
GTCCCGACGG	ACCAGCTCCA	CGCACAGGTC	GATTTCCAGG	TTGCTGACCG	CCGAGCTGAC 1140
CGCGGTGTGC	GACTTGCGCA	GGATCCGCGC	AGCGGAGGAA	ATCGAACCGG	AGGCGATGAC 1200
1210	1220	1230	1240	1250	1260
CTGGAGGAAC	ATGTTACAGT	GATTCAGGTT	ATGAATAGGC	ATCCCTTATT	CCTTTTATTG
GGTGGCGCGT	GCCGCTTCCC	TTGA	1284		

Fig. 7F

10		20		30		40		50	
MARARPCVSI	SVTRCSTASL	TCASRATTRW	WSVACRKVST	AWPMPMARSW					
RWPIRAIDSW	ACNSIPSRFS	PPTASVCWRT	LYSGAARWRS	RSAFGPERRC					
AVSTEARLPG	RRIVETLAAQ	FAQALAGAFE	KATEAALGFQ	RGVVVAIHLG					
VDAARFVQFA	EDCQGTVAQA	FLDEIMRRDA	PSDAGFHQTQ	HVVEVFHEEY					
LVADRPQQVR	MLPGAATEAD	LPVIGQARDA	VQGGIAQRVL	RMGDDERLGV					
260		270		280		290		300	
AEHALVEAGD	LQFLVDGDGD	IDFRVLLDR	RQAIGGRGAY	QADHVEIVEQ					
YAAHRIAERR	RDGGVQQHPE	IARTLVEIEG	DVADQLLVQ	QAAHVRDQAK					
RLLGFDLVA	VPTDQLHAQV	DFQVADRRAD	RGVRLAQDPR	SGGNRTGGDD					
LEEHVHVIQV	MNRHPLFLLL	GGACRFP	427						

Fig. 7G

	10	20	30	40	50	60	
ATGCCTATTTC	ATAACCTGAA	TCACGTGAAC	ATGTTCCCTCC	AGGTCATCGC	CTCCGGTTCG	60	
ATTTCTCTCCG	CTGCGCGGAT	CCTGCGCAAG	TCGCACACCG	CGGTCTAGCTC	GGCGGTCTAGC	120	
AACCTGGAAA	TCGACCTGTG	CGTGAGACTG	GTCCGTCGGG	ACGGCTACAA	GGTCGAACCC	180	
ACCGAGCAGG	CGCTTCGCCT	GATCCCTTAC	ATGCGCAGCC	TGCTGAACTA	CCAGCAGCTG	240	
ATCGGCGACA	TCGCCTTCAA	TCTCAACAAG	GGTCCGCGCA	ATCTCCGGGT	GCTGCTGGAC	300	
	310	320	330	340	350	360	
ACCGCCATCC	CGCCGTCGTT	CTGCGATACG	GTGAGCAGCG	TACTGCTCGA	CGATTTCAAC	360	
ATGGTCAGCC	TGATACGCAC	CTCGCCCGCC	GATAGCCTGG	CGACGATCAA	GCAGGACAAAC	420	
GCGGAAATCG	ATATCGCCAT	CACCATCGAC	GAGGAACTGA	AGATCTCCCG	CTTCAACCAG	480	
TGCGTGCTCG	GCTACACCAA	GGCGTTCGTC	GTGCCCCATC	CGCAGCACCC	GTTGTGCAAT	540	
GCCTCCCTGC	ACAGCATCGC	GAGCCTGGCC	AATTACCGGC	AGATCAGCCT	CGGCAGCCGC	600	
	610	620	630	640	650	660	
TCCGGGCAGC	ATTCTGAACCT	GCTGCGGCCG	GTCAGCGACA	AGGTGCTCTT	CGTGGAAAAAC	660	
TTCGACGACA	TGCTGCGTCT	GGTGGAAGCC	GGCGTCGGAT	GGGGCATCTC	GCCGCATTAT	720	
TTCGTCGAGG	AACGCCCTGCG	CAACGGTACC	CTGGCAGTCC	TCAGCGAACT	GTACGAACCG	780	
GGCGGCATCG	ACACCAAGGT	GTATTGCTAC	TACAACACCG	CGCTGGAATC	CGAGCGCAGC	840	
TTCCGTCGCT	TTCTCGAAAG	CGCCC GCCAG	CGCCTGCGCG	AACTGGGCCG	CCAGCGTTTC	900	
	910	920	930	940	950	960	
GACGATGCGC	CGGCCTGGCA	ACCGAGCCTC	GGTCGAAACT	GCGCAGCGCC	GCTCAGGCC	960	
GAAGGCGCTC	CGCGACCGCC	AACGCGCCGC	ACCAGAGTAG	AGCGTTCTCC	AGCAGACGCT	1020	
GGCCGTGGGT	GGTGA	1035					

Fig. 7H

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Sequence: 34B12 ORF 2 PROTEIN From:: 1 To: 344

10	20	30	40	50	60
MPIHNLNHVN	MFLQVIASGS	ISSAARILRK	SHTAVSSAVS	NLEIDLCVEL	VRRDGYKVEP 60
TEQALRLIPY	MRSLLNYQQL	IGDIAFNLNK	GPRNLRVLLD	TAIPPSFCDT	VSSVLLDDFN 120
MVSLIRTSPA	DSLATIKQDN	AEIDIAITID	EELKISRNFQ	CVLGYTKAFV	VAHPQHPLCN 180
ASLHSIASLA	NYRQISLGSR	SGQHSNLLRP	VSDKVLFVEN	FDDMLRLVEA	GVGWGIAPHY 240
FVEERLRNGT	LAVLSELYEP	GGIDTKVYCY	YNTALESERS	FRRFLESARQ	RLRELGRQRF 300
310	320	330	340	350	360
DDAPAWQPSL	GRNCAAPLRP	EGAPRPPTTR	TRVERSPADA	GRGW	344

Fig. 7I

Sequence: 34B12 ORF 1 From: 1 To: 759

```

      10      20      30      40
      |      |      |      |
ATGCGGCGAG ATGCCCCATC CGACGCCGGC TTCCACCAGA 40
CGCAGCATGT CGTCGAAGTT TTCCACGAAG AGCACCTTGT 80
CGCTGACCGG CCGCAGCAGG TTCGAATGCT GCCCGGAGCG 120
GCTGCCGAGG CTGATCTGCC GGTAATTGGC CAGGCTCGCG 160
ATGCTGTGCA GGGAGGCATT GCACAACGGG TGCTGCGGAT 200
      210      220      230      240
      |      |      |      |
GGGCGACGAC GAACGCCTTG GTGTAGCCGA GCACGCACTG 240
GTTGAAGCGG GAGATCTTCA GTTCCTCGTC GATGGTGATG 280
GCGATATCGA TTTCCGCGTT GTCCTGCTTG ATCGTCGCCA 320
GGCTATCGGC GGGCGAGGTG CGTATCAGGC TGACCATGTT 360
GAAATCGTCG AGCAGTACGC TGCTCACCGT ATCGCAGAAC 400
      410      420      430      440
      |      |      |      |
GACGGCGGGA TGGCGGTGTC CAGCAGCACC CGGAGATTGC 440
GCGGACCCCTT GTTGAGATTG AAGGCGATGT CGCCGATCAG 480
CTGCTGGTAG TTCAGCAGGC TGCGCATGTA AGGGATCAGG 520
CGAAGCGCCT GCTCGGTGGG TTCGACCTTG TAGCCGTCCC 560
GACGGACCAG CTCCACGCAC AGGTCGATTT CCAGGTTGCT 600
      610      620      630      640
      |      |      |      |
GACCGCCGAG CTGACCGCGG TGTGCGACTT GCGCAGGATC 640
CGCGCAGCGG AGGAAATCGA ACCGGAGGCG ATGACCTGGA 680
GGAACATGTT CACGTGATTC AGGTTATGAA TAGGCATCCC 720
TTATTCCTTT TATTGGGTGG CGCGTGCCGC TTCCCTTGA 759

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Fig. 7J

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Sequence: 34B12 ORF 1 S PROTEIN From:: 1 To: 253

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      10      20      30      40
      | | | | | | | | | | | | | | | |
MRRDAPSDAG FHQTQHVVEV FHEEHLVADR PQQVRMLPGA 40
AAEADLPVIG QARDAVQGGI AQRVLRMGDD ERLGVAEHAL 80
VEAGDLQFLV DGDGDIDFRV VLLDRRQAIG GRGAYQADHV 120
EIVEQYAAHR IAERRRDGGV QQHPEIARTL VEIEGDVADQ 160
LLVVQQAHHV RDQAKRLGG FDLVAVPTDQ LHAQVDFQVA 200
      210      220      230      240
      | | | | | | | | | | | | | | | |
DRRADRGVRL AQDPRSGGNR TGGDDLEEHV HVIQVMNRHP 240
LFLLLGGACR FP. 253
```

Fig. 7K

Fig. 7K

pho34B12 ORF1 (L-S) SEQ ID NO:107

```

1  MARARPCVSI SVTRCSTASL TCASRATTRW WSVACRKVST AWPMPMARSW
51  RWPIRAIDSW ACNSIPSRFS PPTASVCWRT LYSGAARWRS RSAFGPERRC
101 AVSTEARLPG RRIVETLAAQ FAQALAGAFE KATEAALGFQ RGVVVAIHLG
151 VDAARFVQFA EDCQGTVAQA FLDEIMRRDA PSDAGFHQTQ HVVEVFHEEY
201 LVADRPQQVR MLPGAATEAD LPVIGQARDA VQGGIAQRVL RMGDDERLGV
251 AEHALVEAGD LQFLVDGDGD IDFRVVLLDR RQAIGGRGAY QADHVEIVEQ
301 YAAHRIAERR RDGGVQQHPE IARTLVEIEG DVADQLLVVQ QAAHVRDQAK
351 RLLGGFDLVA VPTDQLHAQV DFQVADRRAD RGVRLAQDPR SGGNRTGGDD
401 LEEHVHVIQV MNRHPLFLLL GGACRFP*

```

Fig. 8

phoB12 ORF2 SEQ ID NO: 108

```

1  MPIHNLNHVN MFLQVIASGS ISSAARILRK SHTAVSSAVS NLEIDLCVEL
51  VRRDGYKVEP TEQALRLIPY MRSLLNYQQL IGDI AFNLNK GPRNLRVLLD
101 TAIPPSFCDT VSSVLLDDFN MVSLIRTSPA DSLATIKQDN AEIDIAITID
151 EELKISR FNQ CVLGYTKAFV VAHPQHPLCN ASLHSIASLA NYRQISLGSR
201 SGQHSNLLRP VSDKVLFVEN FDDMLRLVEA GVGWGIAPHY FVEERLRNGT
251 LAVLSELYEP GGIDTKVICY YNTALESERS FRRFLESARQ RLRELGRQRF
301 DDAPAWQPSL GRNCAAPLRP EGAPRPPTRR TRVERS PADA GRGW*

```

Fig. 9

36A4 SEQ ID NO: 109

```

1  AAGGGTTTTG GCGGGGTCAT CCGAGTGACC CTGAGCATGC TCCTGGCGAT
51  CTTCTTGTCG GTGCTGCTGG CGCCGGTGCG CATGCTGTTC CACACCCGCT
101 TCGTGCTGGC CGCCTTCCTC GGCTGGTC

```

Fig. 10

36A4 SEQ ID NO:110

```

1  KGFGGVIRVT LSMLLAIFLS VLLAPVRMLF HTRFVLA AFL GW

```

Fig. 11

contig 2507 SEQ ID NO: 111

```

1 CTACTGGGGC AAGCTGAAGA CGCCGTTCAA GCTGAGCTTC TATCACCAGG
51 GCATGCACTT CGACACGCCG GTGAAGATCA ACGAGGTGAC CGCTACCACG
101 GTCAAGCCGA TCAAGTACGA TCGACCAAG TTCGATTTCG GATCCCTGAA
151 GTTCGACGAG AATGCCACCA AGGATCTCGG CTATGCCGGT TTCCGCGTGC
201 TCTATCCGAT CAACAAGGCC GACAAGCAGG ACGAGATCGC CACCTTCCTT
251 GGC GCGAGCT ACTTCCGCGT GGTCGGCAAG GGCCAGGTCT ACGGTCTGTC
301 GGC GCGCGGC CTGGCGATCG ATACCGCGCT GCCTTCGGGC GAAGAGTTCC
351 CGCGCTTCCG CGAATTCTGG ATCGAGCGGC CGAAGCGCAG GACAAGCAAC
401 TGGTGATCTA CGCCCTGCTC GACTCGCCGC GGGCCACCGG CGCCTACCGC
451 TTCGTGCTGC GTCCGGGCAA GGATGCGGTG ATGGATGTCC AGGCCCGCGT
501 GTTCCTCCGC GACAAGGTCA GCAAGCTGGG CCTGGCGCCG CTGACCAGCA
551 TGTACCTGTT CGGCTCCAAC CAGCCGTCCG AGCAGCACA CTTCCGGCCC
601 GAGCTGCATG ACTCCAGCGG CCTGCAGATC CATGCCGGCA ACGGCGAGTG
651 GCTGTGGCGT CCGCTGAACA ATCCGAAGCA CCTGTCGGTG AGCACCTTCA
701 GCGTGGAGAA CCCGAAAGGC TTCGGCCTGC TCCAGCGCGG CCGCGAGTTC
751 TCCC GCTACG AAGACCTGGA TGACCGCTAC GACCTGCGTC CGAGTGCCTG
801 GATCGAGCCG AAGGGCGACT GGGGCAAGGG CACCGTGGA CTGGTGGAAA
851 TCCC GACCCC GGACGAAACC AACGACAATA TCGTCGCGTT CTGGAACCCC
901 GAGACCCAGC CTGAGGTCGG AAAGCCGCTG GACTTCGCCT ACCGCTGCA
951 CTGGACCATG GATGAAGACG AGCTGCACGA CCCGAAATCC TCCTGGGTCA
1001 AGCAGACCAT GCGCTCGGTC GGCGACGTGA AGCAGAAGAA CCTGATCCGC
1051 CAGCAGGACG GCAGACCCGC CCTGGTCGTC GACTTCGAAG GGCCGGCCCT
1101 GAAGGACCTG GCGCCGGACG CGCCGGTGAC CACCCAGGTC AGCACCGACA
1151 GCAACGCCGA GGTGGTGGAG AACAGCCTGC GTTACAACCC GGTCTGAAA
1201 GGCTGGCGCC TGACGCTGCG GATCAAGGTC AAGGATCCGA AGAAGCCGGT
1251 GGAATGCGC GCGGCGCTGG TCGACGAGGC GCAGAAGCCA CTGAGCGAAA
1301 CCTGGAGCTA TCAGCTGCCT GCCGATGAAT AACCATCCA CTACGAAAGC
1351 ACCGCTGGCC GACTACCTCG CTCATCTTCC CCTGGCGGAA GAGGAGCGGG
1401 AGCGCCTTGG CGAGTCCGCT TCCTTCTCCG AGCTGCACGC TCGCCTGGCG
1451 GGAGCGGAAG GCGCCGCTGC CGATGCCGGG GCGATCCCG CCCTGGCCTC
1501 GGTACGCGCC CGCCTGCAGC TGGGCACCCC TGAGCTGGAC GACGCCGAGA
1551 TGTTGCGCGT CGACGCCAG GGTGCGACCT TCCTCAAGAT TTCCCCGCCG
1601 ATCCGCCGTA CCAAGGTGAT TCCCGAGCCC TGGCGCACC AATCCTGGT
1651 GCGCGGCTGG CGTCGGCTGA CCGGACGCAG CAACCCGCCC AAGCCCAAGC
1701 GTGCCCTGCC GCGGGCCCCG TGGCAGCGGG TCGGCTCGCT GCGCCGGTTC
1751 ATCCTGCTGT TGTTGATGCT GGCGCAGACC TCGGTCGCCA CCTACTACAT
1801 GAAAGGCATC CTGCCCTACC AGGGCTGGGC CTTGTCGAC CTGGAGGAGC
1851 TGGCCCAGCA GAGCCTGCTG GATACCGTCC AGCAGGTGCT GCCCTATGTC
1901 ATCCAGTTCG GCATCCTGGC GCTCTTCGCG ATCCTCTTCT GCTGGGTCTC
1951 GGCCGGCTTC TGGACCGCGC TGATGGGCTT CTGGGAGCTG CTCACCGGGC
2001 GTGACCGCTA CCGGATCTCC GGCAGCAGCG CCGGCAGCGA GCCGATCGCC
2051 GCCGACGCCC GCACGGCGAT CGTCATGCCG ATCTGCAACG AAGACGTGCC
2101 GCGGGTATTC GCCGGCCTGC GGGCGACCGT CGAGTCGATG GCCGCCACCG
2151 GCGAGATGGA GCGCTTCGAC TTCTTCGTCC TCAGCGACAC CAACGACCCG
2201 GATATCGCCG TCGCCGAGCA GCAGGCCTGG CTCGAGCTGT GCCGCGAGAC
2251 CAAGGGCTTC GGCAAGATCT TCTACCGTCG CCGCCGGCGC CGGGTGAAGC
2301 GCAAGAGCGG CAACATCGAC GACTTCTGCC GCGGCTGGGG CGGCGACTAC
2351 CGCTACATGG TGGTGATGGA CGCCGACAGC GTGATGAGCG GCGACTGCCT

```

Fig. 12A

2401	GGCCAAGCTG	GTACGCCTGA	TGGAGGCCAA	TCCTGAGGCG	GGGATCATCC
2451	AGACCGCGCC	GAAGGCTCCG	GCATGGACAC	CCTGTATGCG	CGCATGCAGC
2501	AGTTCGCCAC	CCGCGTCTAC	GGCCCGCTGT	TCACCGCCGG	CCTGCACTTC
2551	TGGCAACTCG	GCGAGTCGCA	CTACTGGGGC	CACAACGCGA	TCATCCGCAT
2601	GCAGCCCTTC	ATCGACCACT	GCGCCCTGGC	GCCGTTGCCG	GGCAAGGGCT
2651	CGTTCGCCGG	CGCGATCCTG	TCCCACGACT	TCGTGAGGCG	TGCGTTGATG
2701	CGCCTTGCCG	GCTGGGGCGT	GTGGATCGCC	TACGACTTCG	ACGGCAGCTA
2751	CGAAGAACTG	CCGCCGAACC	TGCTCGACGA	ACTCAAGCGC	GACCGCCGCT
2801	GGTGCCACGG	CAACCTGATG	AACTTCCGCC	TGTTCTTGGT	CAAGGGCATG
2851	CACCCGGTGC	ACCGCGCGGT	GTTCCCTACC	GGGGTCATGT	CCTACCTGTC
2901	GGCGCCGTTG	TGGTTCTTCT	TCCTGGTGCT	TTCCACCGCG	CTGCTGGCGG
2951	TGCACCAACT	GATGGAGCCG	CAGTACTTCC	TGGAACCGCG	GCAGCTGTTT
3001	CCGATCTGGC	CGCAGTGGCA	TCCGGAGAAG	GCCATCGCGT	TGTTCTCCAC
3051	CACCTTGACC	CTGTTGTTCC	TGCCCAAGCT	GCTCAGCGTA	ATGCTGATCT
3101	GGGCAAGGG	CGCCAAGGGT	TTCGGCGGGG	TGATCCGGGT	GACCCTGAGC
3151	ATGCTCCTGG	AGATGTTCTT	CTCGGTGCTG	CTGGCGCCGG	TGCGCATGCT
3201	CTTCCACACC	CGCTTCGTGC	TGGCCGCCTT	CCTCGGCTGG	TCGGTGCAGT
3251	GGAACTCGCC	GCAGCGCGAC	GACGACGCCA	CGCCCTGGAG	CGAGGCGATC
3301	CGCCGGCAGC	CAATGCAGAC	CCTGCTGGGT	ATCGCCTGGA	CCCTGCTGGT
3351	GGCCTGGCTC	AACCCGCGCT	TCCTGTGGTG	GCTGTCGCCG	ATCGTCGGTT
3401	CGCTGATCCT	GTCGATCCCG	GTATCGGTGA	TCTCCAGCCG	GGTGAAGCTG
3451	GGCCTGCGGG	CCCCTACGA	AAAGCTGGTC	CTGATCCCGG	AGAGTACGAC
3501	ACGCCGCGCG	ACTGCGCGCC	ACCGACGAGT	ACACCTACGA	GAACCGCTGG
3551	CATGCGCTCA	AGGATGGCTT	CCTCAAGGCC	GCCGTCGATC	CGTTGCTCAA
3601	CGCCCTGGCC	TGCGCCATGG	GCACGGCTCG	CCACAACCGT	GCGCAGGCCA
3651	TCGAGACGGT	GCGTGGCGAG	CGTATCGGCA	AGGCCATCGA	TAAGGGCCCG
3701	GAACAGCTCG	ACGGCGCCAC	GCGCCTGGCT	CTGTTGAGTG	ACCCGGTAGC
3751	ACTTTCGCGC	CTGCATACGC	GGGTCTGGGA	AGAGGACCGC	GACGACTGGC
3801	TCGGCCGCTG	GCGCAAGGCC	GAGGCGGACG	ACCCCCACGC	CGCCAGCGTA
3851	CCGCTGGCCC	AGGTAGTGCC	CGGCGACGCC	GGCCTGCTGC	CCGCCGCCCA
3901	GTCCTGATCC	CATGCCCCCG	GCGGAACGCC	GCCGGGGGCA	TGGGTCTGTT
4001	TCTTGCTGT	TTTCCCCGTG	CGGCGCTGCT	GTTACCCTGC	GCCGGCAATC
4051	CAGAAAGTCT	CGTATCGTTC	GCCAGCTGAG	GTACTATCGG	CCGCCTTTTG
4101	CGCAGCCGGT	CATGGCCTGC	TGCCCGCCCC	GGACGGCGAC	ACGACGAGAG
4151	CATCCGTTTC	ACGACTGTGT	TTCTAAGACT	GCTGGGGATT	GGGGAATGAA
4201	AAAGTATCTT	GCTTCATTGG	TTCTGGGCGT	CTGCGCCCTG	GTGGGCGTGG
4251	CTTCGGTCCA	GGCGGCCGGC	GCGGTGGAGG	ACGCGGTCAA	GCGCGGCACC
4301	CTGCGGGTCG	GCATGGACCC	GACCTACATG	CCGTTGAGGA	TGACCAACAA
4351	GCGTGGCCAG	ATCATCGGCT	TCGAAGTCGA	CCTGCTCAAG	GCCATGGCCA
4401	AGTCCATGGG	CGTCAAGCTG	GAGCTGGTCT	CCACCAGCTA	CGACGGCATC
4451	ATCCCGGCGC	TGCTGACCGA	CAAGTTCGAC	ATGATCGGCT	CGGGCATGAC
4501	CCTGACCCAG	GAGCGCAACC	TGCGCCTGAA	CTTCTCCGAG	CCCTTCATCG
4551	TGGTCGGCCA	GACCCTGCTG	GTGCGCAAGG	AACTGGAAGG	CAAGATCAAG
4601	TCCTACAAGG	ACCTGAACGA	TCCGCAGTAC	AGCATCACCT	CGAAGATCGG
4651	CACCACCGGT	GAGATCGTTG	CCCCTAAGCT	GATCAGCAAG	GCCAAGTACC
4701	ACGGCTTCGA	CAACGAGCCG	GAAGCGGTGA	TGGACGTGGT	CAACGGCAAG
4751	GCCGACGCCT	TCATCTACGA	CTCGCCCTAC	AACGTGGTGG	CGGTGAGCAA
4801	GTTGCGCGCC	GGCAAGCTGG	TCTACCTCGA	CCAGCCGTTT	ACCTACGAGC
4851	CGCTGGCGTT	CGGCCTGAAG	AAAGGCGACT	ACGACAGCAT	CAATTTTCATC
4901	AACAACCTCC	TCCATCAGAT	CCGCGAAGAC	GGCACCTATC	AGCGCATCCA

Fig. 12B

4951 CGACAAGTGG TTCAAGAACA CCGAGTGGCT GAAGGAAATG GAATGAACCG
 5001 CTGACGGCCC CCGCGAAGGG GGCCGTCGTA CCTGCGCATT CCATCGTTTCG
 5051 AGAGAGTTTC CGTGACCAAG AAGAAACGTT CCGTCTGGCC CTGGCACCTG
 5101 CTGACCGGGC TGATCCTGCT GGTTCATGGCC TGGGCGCTGT GGTTCCTCCAC
 5151 CTCGCTGATT TCCTATGAAA TGGCGTGGGA CCGCGTTTCC GAGTACTTCG
 5201 CTACCAGGCC GAGGAGCCGT TACGGGCCAA CGAGATCGGC CGGGTCGAGG
 5251 CTATCGAGGA ACAGGGCAGG GACGCGCGCG TCACGCTGCT TGGCGAGACG
 5301 GCGAGAAGCA GGTTCGTGACC GTTGCCCAGG ACAGCCTGCA ATTCTCCGAA
 5351 GCGACGACGT GGCCGAGGGC GACGCGGTCG GGGTGACCCG CCACTGGGCC
 5401 GCCGGCACTG CTCTGGGGCC TGTGGACCAC CCTCTGGCTA TCGCTGGTGT
 5451 CCGGTGCCAT CCGTCTGGCT ATCGGCCTGG TCGCCGGCCT CTGCCGGCTG
 5501 TCGAAGAACC CGACCCTGCA CGACCTGTCG ACGATCTACG TCGAGCTGGT
 5551 GCGCGGCACG CCGTTGCTGG TGCAGATCTT CATCTTCTAC TTCTTCATCG
 5601 GCACCGTGCT CAACCTGTCC CGCGAGTTCG CCGGGGTTGC GGCGCTGGCG
 5651 CTGTTACCG GCGCCTACGT GGCCGAGATC ATCCGGGCCG GCGTGCAGTC
 5701 CATCGCCCCG GGACAGAACG AGGCCGCCCG CTCCTGGGC CTGAACGCCG
 5751 GCCAGTCGAT GCGCTACGTG ATCCTGCCGC AGGCTTCAAG CGCGTGCTGC
 5801 CGCCGCTGGC CGGGCAGTTC ATCAGCCTGG TCAAGGACAC CTCGCTGGTC
 5851 TCGGTGATCG CCATCACC GAAGTGCAGT AGCGGCCGCG AGGCGATCAC
 5901 CCACTTCGTT CTCCAATTTC GAGATCTGGT TTCTGCGTCG CCGCGTTGTA
 5951 CCTGCTGTTG AACCTGCCCC TTTTCGCACAT GGCATCCCCA CTGGAGCGGA
 6001 GGCTCGGACA AAGTGATTGA AGTACGCAAC CTGCTGAAGG TCTTCGATAC
 6051 CCGCGGCCAG GTAGTGCGCG CCGTGGACGA CGTGAGTACC CGCGTGGCCA
 6101 GGGGCGAGGT ACTGGTGGTG ATCGGTCCGT CCGGTTCCGG CAAGTCGACC
 6151 TTCCTGCGCT GCCTGAACGG CCTGGAGGAG TTCGACGAAG GCTCGGTGAG
 6201 CATCGACGGC GTCGACCTGG CCGACCCGAG GACCGACATC AATGCCTACC
 6251 GCCGCGAAGT CCGCATGGTG TTCCAGCATT TCAACCTGTT CCCGCACATG
 6301 ACCGTGCTCG AGAACCTCTG CCTGGCCCAA CGCGTGGTGC GCAAGCGCGG
 6351 CAAGGCCGAG CGCGAGGCCA AGGCGCGGGC GCTGCTGGCC AAGGTCGGCA
 6401 TCGGGCAGAA GGCCGACGAA TATCCCTCGC GCCTGTCCGG CGGCCAGCAG
 6451 CAGCGCGTGG CGATCGCTCG CGCGTTGTGC ATGGACCCCA AGGTGATGCT
 6501 GTTCGACGAA CCGACCTCGG CGCTCGATCC GGAGATGGTC GGCGAAGTCC
 6551 TCGACGTCAT GAAGACCCTG GCCGTGGAAG GCATGACCAT GGTCTGCGTG
 6601 ACCCACGAGA TGGGCTTTGC CCGCGAAGTG GCCGACCGCG TGCTGTTCTT
 6651 CGACCACGGC AAGCTGCTGG AGGACGCGCC GCCGGCGCAG TTCTTCGACA
 6701 ATCCGCAGGA CCCGCGGGCC CAGGCCTTCC TCCGCCAGGT CCTCTAGTAC
 6751 CGCGCTAGGC GAACGGCTTG CCCGGCGGCG GCAGGAGCGA CGTCGGACTC
 6801 TGCCGCGCGG CCGGCTGGAT ATCGTTGTCC TCCAGCCAGT CCAGCGCCCA
 6851 TTCGCGCAGG CGCTCGTTCT GGTAGCGGTA CCAGTCCTGC AACAGTCCG
 6901 GGTACTCCAT CAGAGAGTGC TTGAAGGCCT TGAACGGCTT GCGGCTCTGC
 6951 AGCGCGTTG

Fig. 12C

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23A2 DNA SEQ ID NO:112

```
1 CGAGGTTTCC GTCTACGAAG GCACCGGCTC GGTCACCATC CGCGCCGTGT
51 TCCCAACCC GAACAACGAG CTGCTCCCCG GCATGTTTCG TCACGCGCAG
101 TTGCAGG
```

Fig. 13

23A2 peptide SEQ ID NO:113

```
1 EVSVYEGTGS VTIRAVFPNP NNELLPGMFV HAQLQ
```

Fig. 14A

101/133

SEQ ID NO:148

DNA flanking the 23A2 locus.

mexA partial sequence, mexB partial sequence

```

1  ggccaggcaa acgcatggc caccgtgcaa cagctcgacc cgatctacgt cgacgtcacc
61  cagccgtcca ccgccctgtt gcgcatgcgc cgcgaactgg ccagcggcca gttggagcgc
121 gccggcgaca acgctgcgaa ggtctccctg aagctggagg acggtagcca ataccgctg
181 gaaggccgcc tcgaattctc cgaggtttcc gtcgacgaag gcaccggctc ggtcaccatc
241 cgcgccgtgt tccccaaccc gaacaacgag ctgctgcccg gcatgttcgt tcacgcgcag
301 ttgcaggaag gcgtcaagca gaaggccatc ctcgctccgc agcaaggcgt gaccgcgcac
361 ctcaagggcc aggctaccgc gctggtggtg aacgcgcaga acaaggtcga gctgcgggtg
421 atcaaggccg accgggtgat cggcgacaag tggctggtca ccgaaggcct gaacgccggc
481 gacaagatca ttaccgaagg cctgcagttc gtgcagccgg gtgtcgaggt gaagaccgtg
541 ccggcgaaga atgtcgcgtc cgcgcagaag gccgacgccg ctccggcgaa aaccgacagc
601 aagggtgat caaggggatt cgtaatgtcg aagtttttca ttgataggcc cattttcgcg
661 tgggtgatcg ccttgggtgat catgctcgcg ggcggcctgt cgatcctcaa tctgccggtc
721 aaccagtacc cggccatcgc cccgccggcc atcgccgtgc aggtgagcta cccgggcgcc
781 tcggccgaga cggtcagga caccgtggtc caggtgatcg agcagcagat gaacgggatc
841 gacaatctgc gctacatctc ctcggagagt aactccgacg gcagcatgac catcaccgtg
901 accttcgaac agggcaccga ccccgacatc gcccaggtcc aggtgcagaa caagctgcaa
961 ctggccaccc cgctgctgcc gcaggaagtg cagcggccagg ggatccgg

```

Fig. 14B

SEQ ID NO:149

PA14 mexA

```

G QANAMATVQ QLDPIYVDVT QPSTALLRMR RELASGQLER AGDNAAKVS L KLEDGSQYP LEGRLEFSE
VSVDEGTGS VTIRAVFPN PNNELLPGM FVHAQLQEG VKQKAILAP QQGVTRDLK GQATALVVN
AQNKVELRV IKADRVIGD KWLVTGLN AGDKIITEG LQFVQPGVE VKTVPAKNV ASAQKADAA PARTDSKG

```

Fig. 14C

SEQ ID NO:150

PA14 mexB

```

MSKFFIDRPIFAWVIALVIMLAGGLSILNLPVNQYPAIAPPAIA
VQVSYPGASAETVQDTVVQVIEQQMNGIDNLRYSISSENSDGSMTITVTFEQGTDPDI
AQVQVQNKQLQLATPLLPQEVQRQGIR

```

Fig. 14D

PAO1 Phenazine operon SEQ ID NO:114

1 GCAAGCTCAA CTCCAGCAAC AAGGCGGAGG CCACCATGAA GGCTTACGCC
 51 ATCGGCCTGC TCAACTGAAT CGACGCCTCG TCGCCTAGCG AGGCCGCCGC
 101 GCAAGCGTCC GGCCATTAC CGAATGGCCG GATAGCGTTT GCGCCGGTCG
 151 CCTGAGCGCA CGCTTCCCAC CGGCAGCGTT TCCCCGCTGC CCCCTTCGCC
 201 ATTGCGCCCG TCCTCATGTT GTCCGGACGC TAGTCGAACT TTCCGGGCGC
 251 CTGGCAAACC GGCCAAAGAA TAGAACGGAA TCGATGCCCA CACCTTTAAT
 301 TTTTAAGGGT TTTTCCTTTT CAAAAACCGT TATTAAGTTT TCCCCTTTAA
 351 ATCTTGGTAC AACTGGGTTC AGGCGAAACT TCGGTCATGC CATTCGGCAT
 401 TAGTTAAACT TTGAGACTCT CCAAGCGGGA ATTTTGTCCG GAACAGCTTC
 451 ACGGCATTTT TCCGCTTTCA TCCCGATGTT TCTTTCGGTT ATGATTCCAG
 501 TCGATTCGAA CTGCCGGAGT TCCCACCATT CGAGATTACC AACGTTGAAA
 551 AGGGTTTACC GACAACCTGG AATTGCGTCG GCGCAACCGT GCCACGGTCG
 601 AGCACTACAT GCGCATGAAG GGGGCCGAAC GGTACAGCG GCACAGCCTG
 651 TTCGTCGAGG AGGCTGCGCC GGCAACTGGA CCACGGAAAG CGGCGAACCC
 701 CTGGTTTTCC GGGGCCATGA GAGCCTCAGG CGGCTCGCCG AGTGGCTCGA
 751 GCGCTGCTTC CCCGACTGGG AGTGGCACAA CGTGCGGATC TTCGAGACCG
 801 AGGATCCGAA CCACTTCTGG GTCGAGTGCG ACGGGCGCGG CAAGGCGCTG
 851 GTCCCGGGGT ATCCGCAGGG CTATTGCGAG AACCCTACA TCCATTCTTT
 901 CGAACTCGAG AACGGCCGGA TAAAACGCAA TCGCGAGTTC ATGAACCCGA
 1001 TGCAGAAATT GCGTGCATTG GGAATAGCCG TTCCACAAAT AAAACGTGAC
 1051 GGTATTCCCA CCTGATTAAT GTCTATTCCA ATTCAAGAGG AGATATGACG
 1101 ATGCTCGATA ATGCCATTCC TCAAGGTTTC GAAGACGCCG TGGAGTTGCG
 1151 CAGGAAGAAT CGCGAGACGG TGGTCAAGTA TATGAACACC AAAGGCCAGG
 1201 ATCGCCTGCG CCGCCATGAA CTTTTCGTCG AGGACGGCTG TGGCGGTTTA
 1251 TGGACCACCG ATACCGGCTC GCCCATCGTC ATTCGTGGCA AGGACAAGCT
 1301 GGCCGAGCAC GCGGTGTGGT CGTGAAATG CTTCCCGGAT TGGGAGTGGT
 1351 ACAACATCAA GGTCTTCGAG ACCGACGATC CCAACCACTT CTGGGTCGAG
 1401 TGCGACGGCC ACGGCAAGAT CCTCTTCCCC GGCTATCCCG AGGGCTACTA
 1451 CGAGAACCAC TTCCTGCATT CCTTCGAGCT GGACGACGGC AAGATCAAGC
 1501 GCAACCGCGA ATTCATGAAC GTCTTCCAGC AATTGCGCGC CCTGAGCATT
 1551 CCGGTCCCGC AGATCAAACG CGAAGGCATT CCCACCTGAG GCCATCCTGG
 1601 AAGGGGTGAA CTATGGACGA TCTATTGCAA CGCGTACGGC GCTGCGAAGC
 1651 GCTGCAGCAA CCCGAATGGG GCGATCCGTC GCGCCTGCGC GACGTGCAGG
 1701 CGTACCTGCG CGGCAGTCCG GCGCTGATCC GCGCCGGCGA CATCCTGGCC
 1751 CTGCGCGCGA CCCTGGCGCG GGTGCCCCGC GCGGAGGCGC TGGTGGTGCA
 1801 GTGCGGCGAC TGCGCCGAGG ACATGGACGA CCACCATGCC GAGAACGTGG
 1851 CGCGCAAGGC CGCCGTGCTG GAACTGCTGG CCGGCGCCCT GCGCCTGGCC
 1901 GGCCGGCGGC CGATAGATCC GCGTCGGGCG CATCGCCGGG CAGTACGCCA
 1951 AGCCGCGTTC CAAGCCGCAC GAGCAGGTCG GCGAGCAGAC CCTGCCGGTC
 2001 TATCGCGGCG ACATGGTCAA CGGCCGCGAG GCCCATGCCG AACAGCGCCG
 2051 GGCCGATCCG CAGCGGATCC TCAAGGGCTA TGCGGCGGCG CGCAACATCA
 2101 T

Fig. 15

3E8 sequence SEQ ID NO:115

```

1  CGGCGCCGAG GATCCGCTGT TCGAGTTAGG CGCAAGCGTC CGGCCATTCA
51  CGGAATGGCC GGATAGCGTT TGCGCCGGTT GCTTGAGCGC AGCTTCCCAC
101 CGGCAGGGTT TCCCCGCTGC CCCTTTCGCC ATTGCGCCGT CCTCTTGTTG
151 TCCGGCACGC TAGTGCAACT TTCCGGACGC TTGGCAAACC GGCCAAAGAA
201 TAGAACGGAA TCGATGCCCC ACACCTGTAA TTTTAAAGGG GTTATGGCTA
251 TTGCAAAAAA GCGTTTATAA GTTTGTCCCC TGTCAAATCT GGTTACAAC
301 GGGTTTCAGG CGAAACATTC GGTCATGGCA ATTCGGCATT AGTTGAAACT
351 TTGGAGACGC TCCGAAGCGG GCAACTTTTG CCCGGAAAAA GTTTCACGGC
401 AATTTTTCGG GCCTGTCATC CCGATGTCTT CTTTCCAGTA TGGATGCCAG
451 TCGATTTCGAA CTGGCGGAGA TTCGCACCAT GCGAGAGTAC CAACGGTTGA
501 AAGGGTTTAC CGACAACCTG GAATTGCGGC GCGCAACCG TGCCACGGTC
551 GAGCACTACA TGCGCATGAA GGGGGCCGAA CGGTTGCAGC GGCACAGCCT
601 GTTCGTCGAG GACGGCTGCG CCGGCAACTG GACCACGGAA AGCGGCGAAC
651 CCCTGGTTTT CCGGGGCCAT GAGAGCCTCA GGCGGCTCGC CGAGTGGCTC
701 GAGCGCTGCT TCCCCGACTG GGAGTGGCAC AACGTGCGGA TCTTCGAGAC
751 CGAGGATCCG AACCACCTCT GGGTCGAGTG CGACGGGCGC GGCAAGGCGC
801 TGGTCCCGGG GTATCCGCAG GGCTATTGCG AGAACCATA CATCCATTCC
851 TTCGAACTCG AGAACGGCCG GATAAAACGC AATCGCGAGT TCACGAACCC
901 GATGCAGAAA TTGCGTGCAT TGGGAATAGC CGTTCCGCAA ATAAaACGTG
951 ACGGCATTCC CACCTGATTA ATGATTATTC CAATTCAAGA GGAGATATGA
1001 CGATGCTCGA TAATGCTATT CCCCAGGTT TCGAAGACGC CGTGGAGTTG
1051 CGCAGGAAGA ATCGCGAGAC GGTGGTCAAG TATATGAACA CCAAAGGCCA
1101 GGATCGCCTG CGCCGCCATG AACTTTTCGT CGAGGACGGC TGTGGCGGTT
1151 TATGGACCAC CGATACCGGC TCGCCCATCG TCATTCTGTG CAAGGACAAG
1201 CTGGCCGAGC ACGCGGTGTG GTCGCTGAAA TGCCTTCCCG GATTGGGAGT
1251 GGTACAACAT CAAGGT

```

Fig. 16A

3E8 SEQUENCE TAG SEQ ID NO:160

```

1  tatggatgcc agtcgattcg aactggcgga gattcgcacc atgcgagagt accaacggtt
61  gaaagggttt accgacaacc tgggaattgc gcggcgcaac cgtgccacgg tcgagcacta
121 catgcgcatg aagggggccg aacggttgca gcggcacagc ctgttcgtcg aggacggctg
181 cgccggcaac tggaccacgg aaagcggcga acccctgggt ttccggggcc atgagagcct
241 caggcggctc gccgagtggc tcgagcgctg cttccccgac tgggagtggc acaacgtgcg
301 gatcttcgag accgaggatc cgaaccacct ctgggtcgag tgcgacgggc gcggcaaggc
361 gctggtcccg gggatatccg agggctattg cgagaaccac tacatccatt ccttcgaact
421 cgagaacggc cggataaaac gcaatcgcca gttcacgaac ccgatgcaga aattgctgct
481 attgggaata gccgttccgc aaataaaacg tgacggcatt cccacctgat taatgattat
541 tccaattcaa gaggagatat gacgatgctc gataatgcta ttccccaagg tttcgaagac
601 gccgtggagt tgcgcaggaa gaatcgcgag acggtgggtc agtatatgaa caccaaaggc
661 caggatcgcc tgcgcgcgca tgaacttttc gtcgaggacg gctgtggcgg tttatggacc
721 accgataccg gctcgcccat cgtcattcgt ggcaaggaca agctggccga gcacgcggtg
781 tggtcgctga aatgcttccc ggattgggag tggtaacaac tcaaggtctt cgagaccgac
841 gatcccaacc acttctgggt cgagtgcgac ggccacggca agatcctctt ccccggttat
901 cccgaggggt actacgagaa ccacttcctg cattccttcg agctggacga cggcaagatc
961 aagcgcaacc gcgaattcat gaacgtcttc cagcaattgc gcgccctgag cattccggtc
1021 ccgcagatca aacgcgaagg cattcccacc tgaggccatc ctggaagggg tgaactatgg
1081 acgatctatt gcaacgcgta cggcgctgcg aagcgctgca gcaaccgaa tggggcgatc
1141 cgtcgcgcct gcgcgacgtg caggcgctacc tgcgcggcag tccggcgctg atccgcgcgc
1201 gcgacatcct ggccctgcgc gcgacctgg ccgggtcgcc cgcggcgagg cgtggtggt
1261 gcagtgcggc gactgcgccg aggacatgga cgaccacca

```

Fig. 16B

3E8 phzA SEQ ID NO:116

```
1 MREYQRLKGF TDNLELRRRG SAVRVRKRP AIHGMAGZRL RRLERSFPP
51 AGFPRCPFRH CAVLLLSGTL VQLSGRLANR PKNRTESMPH TCNFZGVMAI
101 AKKRLZVCPL SNLVTTGFQA KHSVMAIRHZ LKLWRRSEAG NFCPEKVSRO
151 FFRPVIPMSS FQYGCQSIRT GGDSHHARVP TVERFTDNLE LRRRNRAIVE
201 HYMRMKAER LQRHSLFVED GCAGNWTES GEPLVFRGHE SLRRLAEWLE
251 RCFPDWEWHN VRIFETEDPN HLWVECDGRG KALVPGYPQG YCENHYIHSF
301 ELENGRIKRN REFTNPMQKL RALGIAVPQI KRDIPTZLM IIPIQEEIZR
351 CSIMLFPKVS KTPWSCAGRI ARRWSSIZTP KARIACAAMN FSSRTAVAVY
401 GPPIPARPSS FVARTSWPST RCGRZNAFPD WEWYNIK
```

Fig. 17

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3E8 phzB SEQ ID NO:117

1 MLDNAIPQGF EDAVELRRKN RETVVKYMT KGQDRLRRHE LFVEDGCGGL
51 WTTDTGSPV IRGDKLAEH AVWSLKCLPG LGVVQHGG

Fig. 18A

3E8 PHZA SEQ ID NO:161

MREYQRLKGFTDNLELRRNRATVEHYMRMKAERLQRHSLFVE
DGCAGNWTTESGEPLVFRGHESLRRLAEWLERCFPDWEWHNVRIFETEDPNHLWVECD
GRGKALVPGYPQGYCENHYIHSFELENGRIKRNREFTNPMQKLRALGIAVPQIKRDGIPT

Fig. 18B

PhzB SEQ ID NO:162

MLDNAIPQGFEDAVELRRKNRETVVKYMTKGQDRLRRHELFVEDGCGGLWTTDTGSPVIRGDKLAEHAVWSLKCF
PDWEWYNIKVFETDDPNHFWVECDGHGKILFPGYPEGYENHFLHSFELDDGKIKRNREFMNVFQQLRALSIPVPQIK
REGIPT

Fig. 18C

PhzC SEQ ID NO:163

MDDLQVRRCALQQPEWGDPSRLRDVQAYLRGSPALIRAGDILALRATLAGSPAARRWWCSAATAPRTWTTT

Fig. 18D

PA14 phzR SEQ ID NO:164

phzR DNA sequence : 1161 bp

CGTCGACGAGGCCCGC CATGGGCCAAGGTTTGTGT CCGGAGGCgCTCCCGACGACGATG
 GAGCGTGCGAGAAGAACAATGAGAAAGACCGCCGTGAGGCCCATCGGAGAGCCGTTCTAC
 GGTTCGCGAAAGATCCGGGGCGCCGTCCCCTCCAGCa CAGCGCAGTTCTGCGCGGCGC
 CTCGTGTCCGTGCTCATCGAGAAGTTCTCTTCAGCCTCGTTTCGTGTCGCGCCGGCGGGC
 GGCGAATGGGCTCGACCTCGTCCGGAACACCCGCACAGGGCCGGTGGCGATATGTACTTC
 CAGGTCCGGCTTGATAAAGGGAATTGTCATGAGTGGATAAGACGGAAACAAAAAGAATA
 AAAACGCTGAAGAACCGAATCCTGCCGGGATCGATTGTTGACTGGTGAAGCTGGCATGCA
 TGATGAGAGAGAGGGATATCTCGAGATTTTGTCAAGAATAACAACCGAGGAAGAGTTCTT
 CTCCCTGGTTCTCGAGATATGCGGTAATTATGGATTGCAATTCCTTTTCATTTCGGTGCGCG
 GCGCGCTTTCCCGCTGACCGCGCCTAAATATCATTTCTGTCCAATTACCCAGGGGAATG
 GAAAAGCAGATATATCTCCGAAGACTACACATCCATCGACCCGATCGTGCGCCATGGTCT
 CCTGGAATACACCCCGCTGATCTGGAATGGCGAAGACTTCCAGGAGAACCGTTTCTTCTG
 GGAGGAAGCGCTGCATCACGGCATCCGTACGGCTGGTCGATCCCGGTCCGCGGCAAGTA
 CGGGCTGATCAGCATGCTGTCCCTGGTGCGTTCCAGCGAGAGCATCGCCGCTACGGAAAT
 CCTGGAGAAGGAATCCTTCCTGCTCTGGATCACCAGCATGCTGCAGGCTACCTTCGGCGA
 CCTGCTGGCGCCGCGCATCGTCCCGGAAAGCAATGTGCGCCTGACCGCCAGGGAAACCGA
 GATGCTCAAGTGGACCGCGGTGGGCAAGACCTACGGCGAGATCGGCCTGATCCTGTGAT
 CGACCAGCGCACGGTGAAATTCCATATCGTCAATGCGATGCGCAAGCTCAACTCCAGCAA
 CAAGGCGGAGGCCACCATGAAGGCCTACGCCATCGGCCTGCTCAACTGAATCGACGCCTC
 GTCGCCTAGCGAGGCCGCCGC

Fig. 18E

PA14 PhzR SEQ ID NO:165

PhzR peptide sequence

MHDEREGYLEILSRITTEEEFFSLVLEICGNYGFEFFSFGARAPFPLTAPKYHFLSNYPG
 EWKSRYSISDYTSIDPIVRHGLLEYTPLIWNGEDFQENRFFWEEALHHGIRHGWSIPVRG
 KYGLISMLSLVRSSIESIAATEILEKESFLLWITSMLQATFGDLLAPRIVPESNVRTARE
 TEMPLKWTAVGKTYGEIGLILSIDQRTVKFHIVNAMRKLNSSNKAEMATMKAYAIGLLNZ

Fig. 18F

109/133

34H4 SEQ ID NO:118

```
1  ACCAACATCC TGGTCCTGAG CAACAGCCAG CGCCACGGCC TGGCCGCCGC
51  CTGGCCGATC GTGCTCGGCG CCTGCGCGGC GGTGGCGGCG CTGATCCTGC
101 TGCTCGGGCT CGGCTTGGGC GAGCTGCTGC GGCGCCACCC GTTGCTCCAG
151 CAGGGGCTCG CCTGGCTTGG CGTCGGCTGG CTCAGCTACC TGGCCTGGAG
201 CCTGTTCCGC AGCGCG
```

Fig. 19

33C7 SEQ ID NO:119

```
1  CCACCGAAGT AACGGGTCAG CTCGTCGCAC AACAGGCGTC GTCCTCGGC
51  CTGCATCAGG CTGCCCAGCG GGCCCTGGAA CCAGTCGCGC GCGCCCGGTT
101 GAT
```

Fig. 20

25a12.3 SEQ ID NO:120

```
1  GCGGTGCCCT GGATGTCGTC GTTGAAGCAG CACAGCTCGT CCTTGTAGCG
51  CTCCAGCAAC GGCATGGCAT TGGTCTGGGC GAAGTCCTCG AATTGCAGCA
101 GGACCTTGGG CCACGGCGCT TGATCGCCTG GATGAACAGG TCGACAA
```

Fig. 21

8C12 SEQ ID NO:121

```
1  TATTTGTGTA TAAGNCTCAG GcTctGGAGG GGCCGCTGGG CAGGCNNAAC
51  NNCTTCGCGT NCTNGGCGAC GANTTNCNNA TGCTTCGCNT GCTGCCGGCG
101 TCTCNCCCT CNGTACTAgT CTACGCGTGG ACAACGTGGC
```

Fig. 22

2A8 SEQ ID NO:122

```
1  NATTTGTGTA TAAGAGTCAG GATCGAACGC TTCTCTTCGC CGCAGGAAAG
51  CCACCGCCGA GCTGCTGAAG ATGCTCGAGC GCAAGGGACA AGATCATGGG
101 CTTGCGGCAT NCCNTCTNNA TCGATTCCTN CCCACGCAAC GAAgTGATCA
151 AGGGTTGGTC GAAGCAGCTC GCCGACgAGG TCGGCGACAA GGTCCGTGTT
201 GCGGTTTCCG AGGCCATCGA CAAGACCATG TGGGAGCAGA AGAACTGTTC
251 CCCAACGCCC ACTTCTACCA CGCCTCGGCG TCNCCCNTEC NGTGCTTCCA
301 CCTT
```

Fig. 23

1 tcgttgtaga ggccgaacag gccgagctgc caggtgtcgc cctcg

50E12 SEQ ID NO: 124

```

1 gagcagacct gggtacctat ggcttccttg acccgctgca cgatgatgcc cagcgccgcc
61 ttcagatcct tggcggagtt ctcttccttg acgatcttgc gcagcgtgtt gacgatgctc
121 ggggccttgt ctccgtgttc agtcccgccg cagaaggcgc ggggccagtt ccttcagggc
181 gcggcggtag acctcgcgct tgaaggtcac cacctgtccc agggggtacc agtaactcac
241 ccagcgccag ccgtcgaact cgggcttgct ggtgatatcc atgcgcacgc gcgcctcgtc
301 ggacatcagc cgcagcagga accatttctg cttctggccg atgcacagcg gctggctgtg
361 ggtccgcacc aggcgctgcg gcaaacggta gcgcagccag ccgcgg

```

35A9 SEQ ID NO: 125

```

1 cgcgacagta gcatataatc aatcatgagt gattaattaa ttggcgtttc tgtaacatat
61 ccttatgata tgcggcgccct ttcccttgta aggacgttca gtggccagga aaaccaaaga
121 ggaatcccag aaaaaccgcg acggcatact cgatgcgcgc gagcgggttt tcctggaaaa
181 gggcgtgggc accactgcca

```

pho23 SEQ ID NO: 126

1 togatccaa tgactacaag gacgaaatcc gccagatgc ccgcgacaag gccaacctgg
61 agctggacct gaagggcgac atcggttga gcctgttccc ctggctgggc ctggagc

6G12 SEQ ID NO: 127

```

1 ggataggtgc ggcgaaaac gtacgggacg aaagagcgg tttcccgaat gacgcattct
61 cctgcaagcg caacttgctg gtggtcgata gcaagtaagg cgcgagacat gtcctgaact
121 tcatgggggc tttttcttat agggcggact gtcgattctg ctagctggta atcctttctt
181 tattgtctct gtgtgcgctt tttgtatgga tgtgtcgaat attttgaata tcgccgttca
241 actttatcca gggccgcagt tcagtgattt attttctcga aaagtttggt ttttccaata
301 ttcattgctt atagtctggc cggcc

```

25F1 SEQ ID NO: 128

1	gcaggaaacc	gttctccana	tcttgggcga	gaatcctcgg	cacatgcacg	cgggtccgg
61	cgagcagtc	ggcgacctg	acgaacggtc	ggcagtcttc	ctggggcggc	ggcgcgcca
121	tcaccaccag	gctgcggtcc	cctccctgcc	agcggaata	acgacggaag	ctggcgtcgc
181	tactggccgg	gatcagttcg	gcggggggca	cttccccca	accttcggca	acgaacaact
241	cgggcaaaca	agagtccaac	cagcaattca	gctgctggaa	acgggcatca	tcagacattt
301	acggggttct	ccacggccct	agccgttgcg	caggctcatgc	tttattatcc	agcatctttt

Fig. 24F

Sequences of PA14 50E12 encoding for YgdPPa and PtsPpa

1/1 31/11 61/21 91/31
 GAA AAG GGC CAG ACG CAC GGG GTG ACT CCA TCG GTT GGC GGG TGG GAG GGC CGC GAG AGC CTT TTG CGA AGG CTC CCA CCG GGC CTT GGG AAA aCC CCT AGC CTA CCG GCT TTT GCC

121/41 151/51 181/61 211/71
 GGC CCT GTA TCC TCC CCG CAC GAG TCG CAA AGC CGC GCG TTG CCG CTA TCA CAA GCT TTA TGG AAC AAT GCG GGC ACA TGC GAT TTC GAG GAT GTC CCA GCG TGA TCG ATT CCG ATG GTT
 M I D S D G F

241/81 271/91 301/101 331/111
 TTC GCC CGA ATG TCG GCA TCA TTC TCG CCA ACG AGG CCG GGC AGG TGC TGT GGG CGC GGC GTA TCA ATC AGG AAG CCT GGC AGT TCC CGC AGG GAG GCA TCA ATG ATC GCG AAA CCG CCG
 R P N V G I I L A N E A G Q V L W A R R I N Q E A W Q P P Q G G I N D R E T P E

361/121 391/131 421/141 451/151
 AAG AGG CGC TGT ATC GCG Aat TGA ACG AAG AAG TCG GGC TGG AGG CCG GGG ACG TGC GCA TCC TGG CCT GCA CCC GCG GCT GGC TGC GCT ACC GTT TGC CGC AGC GCC TGG TGC GGA CCC
 E A L Y R E L N E E V G L E A G D V R I L A C T R G W L R Y R L P Q R L V R T H

481/161 511/171 541/181 571/191
 ACA GCC AGC CGC TGT GCA TCG GCC AGA AGC AGA AAT GGT TCC TGC TGC GGC TGA TGT CCG ACG AGG CGC GCG TGC GCA TGG ATA TCA CCA GCA AGC CCG AGT TCG ACG GCT GGC GCT GGG
 S Q P L C I G Q K Q K W F L L R L M S D E A R V R M D I T S X P E F D G W R W V

601/201 631/211 661/221 691/231
 TGA GTT ACT GGT ACC CCC TGG GAC AGG TGG TGA CCT TCA AGC GCG AGG TCT ACC GGC GCG CCC TGA AGG AAC TGG CcC CGC GCC TTC TGG CGC GGG ACT GAA CAC GGA GAC AAG GCC CCG
 S Y W Y P L G Q V V T F K R E V Y R R A L K E L A P R L L A R D *

721/241 751/251 781/261 811/271
 AGC ATG CTC AAC ACG CTG CGC AAG ATC GTC CAG GAA GTG AAC TCC GCC AAG GAT CTG AAG GCG GCG CTG GGC ATC ATC GTG CAG CCG GTC AAG GAA GCC ATG GGT ACC CAG GTC TGC TCG
 M L N T L R K I V Q E V N S A X D L K A A L G I I V Q R V K E A M G T Q V C S

841/281 871/291 901/301 931/311
 GTG TAC CTG CTC GAC ACC GAG ACC CAG CGT TTC GTC CTG ATG GCC ACC GAA GGC CTC AAC AAG CGT TCC ATC GGC AAG GTC AGC ATG GcC CCC AGC GAA GGC CTG GTC GGC CTG GTC GGC
 V Y L L D T E T Q R F V L M A T E G L N K R S I G K V S M A P S E G L V G L V G

961/321 991/331 1021/341 1051/351
 ACC CGC GAG GAG CCG CTC AAC CTG GAG AAC GCC GCC GCC CAC CCG CGC TAC CGC TAT TTC GCC GAG ACC GGC GAG GAG CGC TAC GCG TCG TTC CTC GGC GCG CCG ATC ATC CAC CAT aGG
 T R E E P L N L E N A A A H P R Y R Y F A E T G E E R Y A S F L G A P I I H E R

1081/361 1111/371 1141/381 1171/391
 CCG GTG ATG GGG GTG CTG GTG GTG CAG CAG AAG GAG CGC CGC CAG TTC GAC GAA GGC GAG GAG GCC TTC CTC GTC ACC ATG AGC ACC CAG CTC GCC GGC GGC ATC GCG CAT GCC GAG CCG
 R V M G V L V V Q Q K E R R Q F D E G E E A P L V T M S A Q L A G V I A H A E A

1201/401 1231/411 1261/421 1291/431
 ACC GGT TCG ATC CGC GGC CTG GGC AAG CTC GGC AAG GGC ATC CAG GAA GCC AAG TTC GTC GGC GTG CCC GGC GCC CCC GGG CTG GGG GTG GGC AAG GCG GTG GTG TTG Cct CCG GCG
 T G S I R G L G K L G K G I Q E A K F V G V P G A P G V G V G K A V V V L P P A

1321/441 1351/451 1381/461 1411/471
 GAC CTG GAA GTG GTG CCG GAC AAG CAG GTC GAC GAC ATC GAC GCC GAG ATC GCC CTG TTC AAG CAG GCC CTG GAG GGC GTT CGC GCC GAC ATG CGC GCG CTG TCG AGC AAG CTC GCC AGC
 D L E V V P D R Q V D D I D A E I A L F K Q A L E G V R A D M R A L S S K L A S

1441/481 1471/491 1501/501 1531/511
 CAG ATG CGC AAG GAA GAA CGC GCG CTG TTC GAC GTC TAC CTG ATG ATG CTC GAC GAT GCC TCC ATC GGC AAC GAG GTC AAG CGC ATC ATC CGT ACC GGC CAG TGG GCC CAG GGC GCC CTG
 Q L R K E E R A L F D V Y L M M L D D A S I G N E V K R I I R T G Q W A Q G A L

1561/521 1591/531 1621/541 1651/551
 CGC CAG GTG GTG ATG GAG CAC GTG CAG CGC TTC GAG CTG ATG GAC GAC GCC TAT CTC CGC GAG CGC GCC TCC GAC GTC AAG GAC ATC GGT CGC CGC CTG CTC GCC TAC CTg CAG GAA Gaa
 R Q V V M E H V Q R F E L M D D A Y L R E R A S D V R D I G R R L L A Y L Q E E

1681/561 1711/571 1741/581 1771/591
 CGC AAG CAG AAC CTG ACC TAC CCG CAG CAG ACC ATC ATC GTC AGC GAG GAG CTG TCG CCG GCG ATG CTC GGC GAG GTG CCG GAA GCG CGC CTG GTC GGC CTG GTC TCG GTG CTC GGC TCG
 R K Q N L T Y P E Q T I I V S E E L S P A M L G E V P E G R L V G L V S V L G S

1801/601 1831/611 1861/621 1891/631
 GGC AAC TCG CAC GTG GCG ATC CTC GCC CGT GCC ATG GGC ATC CCC ACG GTG ATG GGG GCG GTC GAC CTG CCG TAC TCC AAG GTC GAC GGT ATC GAC CTG ATC GTC GAT GGC TAC CAC GGC
 G N S H V A I L A R A M G I P T V M G A V D L P Y S K V D G I D L I V D G Y H G

Fig. 24H

113/133

1921/641 1951/651 1981/661 2011/671
GAG GTC TAC ACC AAC CCC TCC GCC GAG CTG GTG CGC CAG TAC AGC GAC GTG GTC GCC GAG GAG CGC GAG CTG AGC AAG GGC CTG GCG GCC CTG CGC GAG CTG CCC TGC GAG ACC CTC GAC
E V Y T N P S A E L V R Q Y S D V V A E E R E L S K G L A A L R E L P C E T L D

2041/681 2071/691 2101/701 2131/711
GGC CAC CGC ATG CCG CTC TGG GTC AAC ACC GGC CTG CTC GCC GAT GTC GCC CGC GCC CAG GAG CGT GGC GCC GAG GGC GTG GGC CTG TAC CGC ACC GAA GTG CCG TTC ATG ATC AAC GAC
G H R M P L W V N T G L L A D V A R A Q E R G A E G V G L Y R T E V P F M I N D

2161/721 2191/731 2221/741 2251/751
CGC TTC CCC AGC GAG AAG GAA CAG CTG GGC ATC TAC CGC GAG CAG CTC AGT GCC TTC CAC CGC CTG CCG GTG ACC ATG CGC ACC CTG GAT ATC GGC GGC GAC AAG GCG CTG TCC TAC TTC
R F P S E K E Q L A I Y R E Q L S A P E P L P V T M R T L D I G G D K A L S Y F

2281/761 2311/771 2341/781 2371/791
CGC ATC AAG GAA GAC AAC CCG TTC CTC GGC TGG CGC GGC ATC CGC GTC ACC CTC GAC CAC CGC GAG ATC TTC CTG GTC CAG ACC CGC GGC ATC CTC AAG GCC AGC GAA GGA CTG GAC AAC
P I K E D N P F L G W R G I R V T L D H P E I F L V Q T R A M L K A S E G L D N

2401/801 2431/811 2461/821 2491/831
CTG CGC ATC CTG CTG CCG ATG ATC TCC GGC ACC CAC GAG CTG GAA GAG GCC CTG CAC CTG ATC CAC CGC GGC TGG GGC GAG GTG CGC GAC GAG GGC GTG GAC ATC GCC ATG CCG CCG ATC
L R I L L P M I S G T H E L E E A L H L I H R A W G E V R D E G V D I A M P P I

2521/841 2551/851 2581/861 2611/871
GGC ATG ATG GTC GAG ATT CCC GCC GGC GTG TAC CAG ACC CGC GAG CTG GCC CGT CAG GTC CAC TTC CTT TCG GTC GGT TCG AAC GAC CTG ACC CAG TAC CTG CTG GCG GTC GAC CGC AAC
G M M V E I P A A V Y Q T R E L A R Q V D F L S V G S N D L T Q Y L L A V D R N

2641/881 2671/891 2701/901 2731/911
AAT CCG CGG GTC GCC GAC CTC TAC GAC TAC CTG CAT CCG GCC GTG CTG CAT GCG TTG AAG AAG GTG GTC GAC GAT GCC CAC CTG GAA GGC AAG CCG GTG AGC ATC TGC GGC GAG ATG GCC
N P R V A D L Y D Y L H P A V L H A L K X V V D D A H L E G K P V S I C G E M A

2761/921 2791/931 2821/941 2851/951
GGC GAT CCC GCG GCT GCC GTG CTG ATG GCG ATG GGC TTC GAC AGC CTG TCG ATG AAC GCC ACC AAC CTG CCC AAG GTG AAG TGG CTG CTG CGC CAG ATC ACC CTG GAC AAG GCC CCG
G D P A A A V L L N A M G F D S L S N N A T N L P K V K W L L R Q I T L D K A R

2881/961 2911/971 2941/981 2971/991
GAC CTG CTC GGC CAG TTG CTC ACC TTC GAC AAC CCG CAG GTC ATC CAC AGC TCG CTG CAC CTG GCG TTG CGC AAC CTC GGC CTG GGT CGC GTG ATC AAC CCG GCG GCT ACC GTC CAG CCC
D L L G Q L L T F D N P Q V I E S S L H L A L R N L G L G R V I N P A A T V Q P

3001/1001
TGA TTT TCC C
*

Fig. 24I

Sequence of PA14 35A9 encoding mirRPa

1/1 31/11 61/21 91/31
 GTC GAT TTG GAA CAG CAC GGT GCC GGC GCG GAC TgC CTG GCC TTC CTC GTA CAG GCG AGC GGT GAC GAT GCC GGC GAC GCG CCG CgC cTC gGC CTG GCG GTA CgC TTC CAG GCG TCC

121/41 151/51 181/61 211/71
 GGG CAG CTC GCT GGT GAT GCC gGG CCG CCG CCT GGC GAC GAT CAC GCC GAC CTC GCG GGG GGC CTC CCG AGT CTT CCC GGT GTC CCG TGC TTC TTA GCA GCC CAG CAG GAA TAG GGC

241/81 271/91 301/101 331/111
 GAC CAG GGC CCG CAG CAG CCC GCG CAG CGA GCC GGT CCA TTG GAT GTG CAT GGG TGT CCC TGG ATT CGT GAA CTC GCG AGC TTG CCC GGG AAg GGG CAC CCG AAC TCA CGA GCG GCG CGA

361/121 391/131 421/141 451/151
 CAG TAG CAT ATA ATC AAT CAT GAG TGA cTA ATT AAT TGG CGT TTC TGT AAC ATA TCC TTA TGA TCT GCG GCG CCT TTC CCT TGT GAG GAC GTT CAG TGG CCA GGA AAA CCA AAG AGG AAT
 M A R K T K E E S

481/161 511/171 541/181 571/191
 CCC AGA AAA CCC GCG AtG GCA TAC TCG ATG CCG CCG AGC GGG TTT TCC TGG AAA AGG GCG TGG GCA CCA CTG CCA TGG CCG ACC TGG CCG ACG CCG CCG GGG TTT CTC GCG GTG CCG TCT
 Q K T R D G I L D A A E R V F L E K G V G T T A M A D L A D A A G V S R G A V Y

601/201 631/211 661/221 691/231
 ACC GCC ACT ACA AGA ACA AGA TCG AGG TCT GTC TGG CGA TGT GCG ACC GCG CCT TCG GCC AGA TCG AGC TAC CCG AtG AAA ACG CCA GGG TGC CCG CCG TGG Aca TCC TCC TGC GCG CCG
 G H Y K N K I E V C L A M C D R A F G Q I E V P D E N A R V P A L D I L L R A G

721/241 751/251 781/261 811/271
 GCA TGG GCT TTC TCC GCC AGT GCT GCG AaC CCG GTT CCG TGC AGC GGG TGC TGG AGA TCC TCT ACC TCA AGT GCG AAC GCA GCG ACG AGA ACG AGC CCG TGT TGC GCC GCC GCG AGC TGC
 M G F L R Q C C E P G S V Q R V L E I L Y L K C E R S D E N E P L L R R R E L L

841/281 871/291 901/301 931/311
 TCG AGA AGC AGG GGC AAC GCT TCG GCC gaC GGC AGA TCC GCC GGG CCG TGG AgC GCG GCG AAC TGC CCG CCG GGC TGG ACG TCG AGC TGG CCA GCA TCT ATC TGC AAT CCG TgT GGC ACG
 E X Q G Q R F G R R Q I R R A V E R G E L P A R L D V E L A S I Y L Q S L W D G

961/321 991/331 1021/341 1051/351
 GCA TCT GCG GCA CCC TGG CCT GGA CCG AGC GCT TGC GCG ACG ATC CCT GGA gCC GCG CCG AAC GCA TGT TCC CCG CCG GCC TCG ALa GCC TGC GCA GTT CTC CCT ACC TcT TGC TGG CCG
 I C G T L A W T E R L R D D P W S R A E R M F R A G L D S L R S S P Y L L L A D

1081/361 1111/371 1141/381 1171/391
 ACG CCT GAG GGC GTC AAT CGT CCG CCA TCA GGT GCC TGC GCT GGT CCT CCG CCG CCG GCA CCA GCC GCT GGG CGT CcT CCT CCG TGA TGT GCA GGC GCT TGC Cat CGA TGT AGA GCA
 A *

1201/401 1231/411 1261/421 1291/431
 CCG ACA GGC GCG CCT CCG CGT CCG TAC CGA TGC GCA GGC TGT CGA CCG GCG CCG GAT GCC GGC TGC CTT CGA TCT CCA CCG TGC AGA tGC CTT GTT CCG AAT CGA TTT CGA TGG ACA TGG

1321/441 1351/451 1381/461 1411/471
 Gaa CTT CCc GTT Ttc TCC GCC TAC CTT GGG TGG ACC CCG GGC ATC CCG GCG GGT TCT GTC ACG GTA GCT TCA CCG CAG CGT CAC GCG CCT GCC ACC GCG CTT GGC TGC AAT CGT CCG CAG

1441/481 1471/491 1501/501
 AGA aGG CGA GGC CAG CCG AGG ACG ACG CCA TGC GGC TAT GCG TGA TTG GTG CCG GCT ATG TGG GAC TGG TGA

Fig. 24J

115/133

Sequences of PA14 25Fl encoding for orfT, OrfU and DjlAPa

1/1 31/11 61/21 91/31
CGA GGA ATC CAG TCG AGG TGC GAg TAG TCC GCA CTG CCG GAT CTC AGC GCG CGA CCA CCG GAC TCG GTG ACC AGG CCG TGG GTC GGC TCT GCC TCG AGG GTT TCG CCT CCG CTG CCG GAC

121/41 151/51 181/61 211/71
ACG CTG CTG CCC GCC GCG GCG GTG CTG ACC GAG GTC GCG GTA TGC GCC GGG CCG GGT GGC AGG TTG GCA TTG CCG TTC TGC AGC GGG GAG CAA TCC CAG CCG CCG GTG GCC GAT ACC TTG

241/81 271/91 301/101 331/111
CAG TCG AAC TGA TCG GCG GCC TGT ACA GTC AAT GCT GCG ACC GGC TGC AGA GCC AGC AGG CTG CCG GTG ACC AGC AGG GGA AAC TTT CTT CGA AAC AGC AGG GAT TTC ACT GCC ATC TTG

361/121 391/131 421/141 451/151
TTA ATC CCG GCT TCC TGC GCG CCA TCG GCC CCG TGG GCC GCA CCG CTC TCG ATG GGC TGA AAA AGA TGC TGG ATA ATA AAG CAT GAC CTG CCG AAC GGC TAG GGC CGT GGA GAA CCC CGT

481/161 511/171 541/181 571/191
AAA TGT CTG ATG ATG CCC GTT TCC AGC AGC TGA ATC GCT GGT TGG ACT CTT GTT TGC CCG AGT TGT TCG TTG CCG AAG GTT GGG GGG AAG TGC CCC CCG CCG AAC TGA TCC CCG CCA GTA
M S D D A R P Q Q L N R W L D S C L P E L F V A E G W G E V P P A E L I P A S S

601/201 631/211 661/221 691/231
GCG ACG CCA GCT TCC GTC GTT ATT TCC GCT GCG AGG GAG GGG ACC GCA GCC TGG TGG TGA TGG ACG CCG CCG CCG CCC AGG AAG ACT GCC GAC CGT TCG TCA AGG TCG CCG GAC TGC TCG
D A S P R R Y F R W Q G G D R S L V V M D A P P P Q E D C R P F V K V A G L L A

721/241 751/251 781/261 811/271
CCG GAG CCG GCG TGC ATG TGC CGA GGA TTC TCG CCC AGG ATC TGG AGA ACG GTT TCC TGC TGC TCA GTG ACC TGG GCC GGC AGA CCT ACC TCG ACG TGC TTC ATC CCG GAA ATG CCG ACG
G A G V H V P R I L A Q D L E N G F L L L S D L G R Q T Y L D V L H P G N A D E

841/281 871/291 901/301 931/311
AGC TGT TCG AAC CCG CCC TGG ATG CCG TGA TCG CCT TCC AGA AGG TCG ATG TCG CCG TGC TCC TGC CTG CCT ACG ACG AAG CCG TGC TGC GCC GCG AGC TGC AGC TGT TCC CCG ACT GGT
L F E P A L D A L I A F Q K V D V A G V L P A Y D E A V L R R E L Q L F P D W Y

961/321 991/331 1021/341 1051/351
ACC TGG CCC GCC ACC TCG GCG TGG AGC TGG AGG GCG AGA CCG TGG CCC GCT GGC AGC TGT GCG ACC TGC TGG TAC GCA GCG CCG TGG AGC AAC CCG GGG TGT TCG TCC ATC CCG ACT
L A R H L G V E L E G E T L A R W Q R I C D L L V R S A L E Q P R V F V H R D Y

1081/361 1111/371 1141/381 1171/391
ATA TGC CCG GCA ACC TGA TGC TCA GCG AGC CCA ACC CCG GCG TCC TCG ACT TCC AGG ACG CCC TGC ACC GCG CCG TCA CCT ACG ATG TCA CCT GCC TGT ACA AGG ATG CCT TCG TCA GTT
M P R N L M L S E P N P G V L D F Q D A L H G P V T Y D V T C L Y K D A F V S W

1201/401 1231/411 1261/421 1291/431
GGC CCG AGC CCG GCG TGC ATG CCG CCG TGA GTC GTT ACT GGA AGA AGG CGA CCT GCG CCG GCA TCC CCG TGC CCG CAA GCT TCG AGG ACT TCC TCC GCG CCA GCG ACC TGA TGG GCG TGC
P E P R V H A A L S R Y W K K A T W A G I P L P P S F E D F L R A S D L M G V Q

1321/441 1351/451 1381/461 1411/471
AGC GCC ACC TGA AGG TGA TTG GCA TCT TCG CCC GTA TTT GTC ACC GCG ACG GCA AGC CCG ACT TGG GTG ACG TGC CAC GCT TCT TCC GTT ATC TGG AAA CCG CCG TGG CCG GCC GTC
R H L K V I G I F A R I C H R D G K P R Y L G D V P R F F R Y L E T A V A R R P

1441/481 1471/491 1501/501 1531/511
CCG AGC TGG CCG AAC TGG GCG AGC TGC TGG CCT CCG TGC CCG AGG GAG CCG AGG CAT GAA GGC GAT GAT CCT CCG CCG CCG CCG TGG CGA GCG CAT GCG GCC GAC CAC CCT GCA CAC GCC
M K A M I L A A G R G E R M R P T T L H T P E L A E L G E L L A S L P Q G A E A

1561/521 1591/531 1621/541 1651/551
CAA GCC GCT GAT CGA GGC CCG CCG GGT GCC ATT GAT CGA GCG TCA GTT GCT GGC GCT GCG CCA GCG CCG AGT CGA CGA CTG GGT GAT CAA CCA TGC CTG GCT TGG CGA GCA GAT CGA GGC
K P L I E A A G V P L I E R Q L L A L R Q A G V D D W V I N H A W L G E Q I E A

Fig. 24K

1681/561 1711/571 1741/581 1771/591
 CTA TCT CGG CGA CGG CTC GCG CCT GGG CGG GCG GAT CGC CTA TTC ACC CGA GGG AGA ACC GCT GGA AAC CGG CGG TGG AAT CTT CCG CGC CCT GCC GTT GCT CGG CGA GCA GCC GTT CCT
 Y L G D G S R L G G R I A Y S P E G E P L E T G G G I F R A L P L L G E Q P F L

1801/601 1831/611 1861/621 1891/631
 GTT GCT CAA CGG CGA TGT CTG GAG CGA CTT CGA CTA CTC TCG GCT GCA TCT TGC CGA CGG CGA CCT GGC GCA TCT GGT GCT GGT CGA CAA CCC GGC GCA CCA TCC CGC CGG CGA TTT CCA
 L L N G D V W S D F D Y S R L H L A D G D L A H L V L V D N P A H H P A G D F H

1921/641 1951/651 1981/661 2011/671
 CCT GGA TGC CGG CGG ACG GGT GGG CGA GAC CGG CGA AGC GGG CGG CAA CCT GAC CTA CAG CGG GAT CGC GGT ACT GCA TCC CGC GCT GTT CGA GGG CTG CCA GCC GGG CGC CTT CAA GCT
 L D A G G R V G E T R E A G G N L T Y S G I A V L H P A L P E G C Q P G A F K L

2041/681 2071/691 2101/701 2131/711
 GGC GCT GCT ATT GCG CAA GGC CAT CGC CGG GCG GGT CAG CGG CGA ACA CTA TCG TGG CGA GTG GGT CGA CGT CGG TAC CCA CGA GCG CCT GGC GGA AGT CGA GCG ATT GCT GGC GGA
 A P L L R K A I A A G R V S G E H Y R G Q W V D V G T H E R L A E V E R L L A E

2161/721 2191/731 2221/741 2251/751
 GCA CGC CTG AGA TGC TCT GGC CCG CTA CGC TGA TCG GAG CGG GAG CGG GCT GGG CCC TGG CCA GCA TCC CCG GCG CCC TGC TCG GCG GCC TGC TGG GGC AAC TGC TGG ACC GCA GGT TGC
 H A * M L W P A T L I G A G A G W A L A S I P G A L L G G L L G Q L L D R R L R

2281/761 2311/771 2341/781 2371/791
 GGC TGG AGT CTT GGC GCG GCC TGC TGG GCG GCT TGC GCG GCG GGG CGG TGA ACG ATG AGG CGC ACC TGC TGT TCC AGT TGC TCG GCT ATC TGG CCA AGA GCG GCG GCG GGG TGG AGG AGA
 L E S W R G L L A R L R G R A V N D E D D L L F Q L L G Y L A K S G G R V E E M

2401/801 2431/811 2461/821 2491/831
 TGC ATA TCC GCC AGG CGC GCG AGG AGA TGG CGT TGC GCA AGC TCG ATA GGC GAG CCC AGC GGC GTG CCA TCG CGT CTT TCG GCA AGG CCA AGC CGG GCA TCG CCC ATC TGC AGG CGG AGG
 H I R Q A R E E M A L R K L D R R A Q R R A I A S F G K G K A G I A H L Q A E V

2521/841 2551/851 2581/861 2611/871
 TCG CGC GTC TGA AGG GCG AAC GTG CGG AGG CAG TAT TGC TCG CCT GCT GGC GGA TGG CTT GGG CTG GCG GCG TGC TCA GCC AGT CGG CGC GAC AAC TGG TGT TGC AAT GGG GGC GCT GGC
 A R L K G E R A E A V L L A C W R M A W A G G V L S Q S A R Q L V L Q W G R W L

2641/881 2671/891 2701/901 2731/911
 TGG GTT GGT CGG CGG AGC GAA CGG AAC GCT TGT CCG CGC GGG TCA TGC CGA AGC GGA CGC GCG CTG TCG CCC GGG ATA GCT ACC GTG AGG CCC TGC TGC TCG GCG TGG AGG CGG GAA
 G W S A E R T E R L S A R V M P K R T R A V A R D S Y R E A L L L L G V E A G S

2761/921 2791/931 2821/941 2851/951
 GCG AGC CGG CGC TGA TCA AAC GCG CTT ATC GCA AGC TGA TCA GCC AGC ATC ATC CGG ACA AAC TGG CGG GAG CGG GCG CCA GCG TCG AGC GCG TGC GTG CGG CTA CGG AGA AAA CCC GTG
 E P A L I K R A Y R K L I S Q H H P D K L A G A G A S V E R V R A A T E K T R E

2881/961 2911/971 2941/981 2971/991
 AAT TGC AGG CGG CCT ACG CCC TGG TCC GAG AGC GTG AGG GGT TCC GCT GAT CAC TCC GCA GGT TTC TGC GCA TCG GCC TGC AGG TGA AGA CTG AGC CAG CGG CGG ATT CGT CGG TAC AGT
 L Q A A Y A L V R E R E G F R *

3001/1001 3031/1011 3061/1021 3091/1031
 TGC TCC TGC TCC GCC TTG GGG TCG GCC GGT AGA GCC TGC ATC GCG ATT TGT ACG TAG GCG GGT TTC TGC CGC TTG CCG GCC TGC ATG CGC AGC CTG GCC GCC TCG CGG TCG GCG CG

Fig. 24L

PhnA and PhnB SEQ ID NO: 129

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1 CTGCAGCGTC TGCCGACCCT GCTGCAACTG ATCCCGGGAC ACGGCGGCCCT
51 GCTGCGGGGG CGGCTGGCCG CGGATGGGGC CGAGTCGGCC TATACCGAGT
101 GTCTGCGCCT GTGCCGACGG TTGCTCTGGC GCCAGTCCAT GGGCGAGTCC
151 CTCGACGAAC TGAGCGAGGA GCTGCACCGC GCCTGGGGAG GGCAGAGCGT
201 CGACTTCCTG CCCGGCGAAC TGCACCTGGG GAGCATGCGC CGGATGCTGG
251 AGATTCTCTC CCGCCAGGCG CTGCCTCTGG ACTGAGGCGG AACATCCATT
301 GCGGCGATCG CGCCGACGG CTGCGGTCGC AATTGGGGGA AATGGGGGTA
351 TCGATGATGA ATATGCCGTT GCGCGCTAGC GTCGCGCAGG CCAGTCGCCC
401 ATGGGCGCGG GGAGGTGGCT CGTGAGTGGG GTTGGCTATC GACTGGAAGA
451 AAGTCTGGAG TACCGCACGC TGGTGCCGGA GCGCTGTCTG ATCTGGCGCA
501 TGGCTGGCGC CAACCGGATG CTGTTCGACT GCTTCGACGT GGACAGCAAG
551 GCTGCGCGGC GTAGCGTGGC GATCCTTTCC AGCTGCCTGC GCATCGAGTG
601 CTGGGGGCGC GATGTGGTGC TGCGGGCGTT GAACTCCAAC GGACGCGCCT
651 TGCTGGCGCC GTTGAGCGAG GCCTGTCCGG CCCAGGTCAC CTGCTTGCGT
701 GACGGCGACA CCCTGCACTG GCGCTTCCCC CCGGAAGAGC CGCATGCGGA
751 CGAGTGGCGA CGCCTGCATG GCCTGTCCAG CCTGGAGGCG CTGCGCCGCG
801 TGCTCGGAAC GCTGGGCGAC GCGGAGGGGC CTGCGCTGCT GGGCGGCCTG
851 TTCAGTTTCG ACCTGGCCGA GCAGTTCGAA CCCTTGCCGG CGCCGGCCGA
901 ACCTGCGCGG CATTGCCCGG ACTACCTGTT CCTGGTGCCG GAGTTGCTGC
951 TGGATATCGA TCACCTGGCG CGCCGGAATT CGCTGCAAGC GTTCGTCCAC
1001 GATCCGGCCG GGCACGACCG GTTGGCCGCC AGCCTGCGCC AATGTGCCGA
1051 CGAATTCCAT GGCGCCGTGG AGGAGGCTTC CGAGTCGCCG GTGGCAGGCG
1101 TACGGGCCCG CAACTACCAG GTCGACCTGG ACGATGCGAG CTTTGCCCGC
1151 CAGGTAGAAC GCCTGCAGGC CCACGTGAGG GCCGGCGACG TGTTCCAGAT
1201 CGTACCTTCG CGCAGCTTCA GCATGCCGTG CGCGGACCCC TGGCGGGCCT
1251 ATCGCCAGTT GTGCCTGCGC AACCCAGCC CGTACCCTT CTTCTCGAT
1301 GCGGGGGACT TCTGCCTGTT CGGCGCTTCG CCGGAGTCGG CATTGAAGTA
1351 CGACGCGGAG AGTCGCGAGG TGGAAGTCTA TCCCATTGCC GGCACCCGCC
1401 CGCGCGGATG CGATGCCCGG GCGGCCATCG ATGCGGAACT GGACAATCGC
1451 CTGGAAGCGG AGTTGCGCCT GGATGCCAAG GAGATCGCCG AGCACATGAT
1501 GCTGGTCGAC CTGGCGCGCA ACGATCTGGC GCGCGTCTGC CGCAGCGGTA
1551 CCCGGCAGGT GCGCGACATG CTCAAGGTCG ATCGCTACAG CCACGTGATG
1601 CACCTGGTCT CGCGCGTGGC TGGCGAACTG CACGGCGAAC TGGATGCGCT
1651 GCATGCCTAC CGTGCCCTGCC TGAACATGGG CACCCTGGTC GGC CGCGCCGA
1701 AGGTCCGTGC CATGCAGTTG CTGCGGCAGT ACGAGGATGG CTATCGCGGC
1751 AGCTACGGTG GTGCGATCGG CATTCTCGAC AGCGCCGGCA ACCTCGATAC
1801 CAGCATTGTC ATCCGCTCCG CCGAGGTCCG CGAAGGTATC GCGCGGGTTC
1851 GGGCAGGCGC CGGCGTGGTG CTGGATTCCG ATCCACGGCT GGAGGCCGAG
1901 GAAACCCGCA ACAAGGCGCT GGCGGTGCTG ACCGCCGTGG CCGCTGCCGA
1951 ACGCGAAAGG GGAGAGCGCG ATGCGCATCA CGCTGTTGGA TAACTTCGAT
2001 TCCTTCACCT ACAACCTGGT CGAGCAGTTC TGCCTGCTCG GCGCGGAGGT
2051 CCGGGTGATG CGCAACGATA CGCCGTTGCC GACGATCCAG GCGGCATTGC
2101 TGGCCGACGG TTGCGAACTG CTGGTGCTGT CGCCGGGGCC CGGTCGGCCG

```

Fig. 25A

2151 GAAGACGCCG GCTGTATGCT GGAATTGCTC GCCTGGGCCC GCGGGCGCTT
2201 GCCGGTGCTC GGCGTCTGCC TCGGCCACCA GGCGCTGGCG CTGGCCGCCG
2251 GTGGCGCGGT GGGCGAGGCG AGGAAGCCGC TGCATGGCAA GAGCACGTCC
2301 CTGCGTTTCG ATCAGCGTCA CCCGCTGTTC GACGGCATCG CTGACCTGCG
2351 CGTCGCGCGC TACCACTCGC TGGTGGTCAG TCGCCTGCCG GAAGGTTTCG
2401 ACTGCCTGGC CGATGCCGAT GGCGAGATCA TGGCGATGGC CGATCCGCGC
2451 AATCGACAGC TGGGCTTGCA ATTCCATCCC GAGTCGATTC TCACCACCCA
2501 CGGCCAGCGT CTGCTGGAGA ACGCTCTACT CTGGTGCGGC GCGTTGGCGG
2551 TCGCGGAGCG CCTTCGGGCC TGAGCGGCGC TGCGCAGTTT CGACCGAGGC
2601 TCGGTTGCCA GGCCGGCGCA TCGTCGAAAC GCTGGCGGCC CAGTTCGCGC
2651 AGGCGCTGGC GGGCGCTTTC GAGAAAGCGA CGGAAGCTGC GCTCGGATTC
2701 CAGCGCGGTG TTGTAGTAGC AATACACCTT GGTGTCGATG CCGCCCGGTT
2751 CGTACAGTTC GCTGAGGACT GCCAGGGTAC CGTTGCGCAG GCGTTCCTcG
2801 ACGAAATAAT GCGGCGaGAT GCCCCATCCG ACGCCGGCTT CCACCAGACG
2851 CAGCATGTCG TCGAAGTTTT CCACGAAGAG CACCTTGTCG CTGACCGGCC
2901 GCAGCAGGTT CGAATGCTGC CCGGAGCGGC TgCCGAGGCT GATCTGCCGG
2951 TAATTGGCCA GGCTCGCGAT GCTGTGCAGG GAGGCATTGC ACAACGGGTG
3001 CTGCGGATGG GCGACGACGA ACGCCTTGGT GTAGCCGAGC ACGCACTGGT
3051 TGAAGCGGGA GATCT

Fig. 25B

PhnA protein SEQ ID NO:130

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1  MGARRWLVSQ VGYRLEESLE YRTLVPPEALS IWRMAGANRM LFDCFDVDSK
51  AARRSVAILS SCLRIECWGR DVVLRALNSN GRALLAPLSE DCPAQVTCLR
101 DGDTLHWRFP QEESHADWR RLHGLSSLEA LRRVLGTLGD AEGPVLLGGL
151 FSFDLAEQFE PLPAPAEPR HCPDYFLVP ELLLDIDHLA RRTSLQAFVH
201 DPAGHDLAA SLRQCADEFH GAVEEASESP VAGVRAGNYQ VDLDDASFA
251 QVERLQAHVR AGDVFQIVPS RSFSMPCADP WRAYRQLCLR NPSPYRFFLD
301 AGDFCLFGAS PESALKYDAE SREVELYPIA GTRPRGRDAR GAIDAELDNR
351 LEAELRLDAK EIAEHMMLVD LARNDLARVC RSGTRQVRDM LKVDYRSHVM
401 HLVSrvAGEL HGELDALHAY RACLNMGTLV GAPKVRAMQL LRQYEDGYRG
451 SYGGAIGILD SAGNLDTSIV IRSAEVREGI ARVRAGAGVV LDSDPRLAE
501 ETRNKALAVL TAVAAAERER GERDAHHA

```

Fig. 26

PA14 degP SEQ ID NO:131

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1  CGTCCGATTC GGCCTGAGTC TTTCTCTTCC CTCGAACATC ACGGGAGCTG TAGTCGATGC
61  ATACCCTAAA ACGCTGTATG GCTGCGATGG TGGCCTTGCT GGCCTTGAGC CTGGCGATGA
121 CGGCCCCGGG AGAACTGCCG GACTTCACGC CTTTGGTCGA ACAGGCGTCG CCGGCGGTGG
181 TGAATATCAG TACGCGGCAG AAGCTGCCGG ATCGCGCCAT GGCGCGCGGG CAGCTGTCTGA
241 TCCCCGACCT CGAAGGGCTG CCGCCGATGT TCCGCGACTT CCTCGAGCGC ACGATCCCGC
301 AGGTTCGCG CAATCCGCGC GGCCAGCAGC GCGAGGCGCA ATCGTGCGG TCCGGCTTCA
361 TCATCTCCAA CGACGGCTAC ATCCTCACCA ACAATCACGT CGTGGCCGAT GCCGACGAGA
421 TCCTGGTGCG CCTGTCCGAC CGTAGCGAGC ACAAGGCCAA GCTGGTCGGC GCGGACCCGC
481 GCAGCGACGT GCGGTGCTG AAGATCGAGG CGAAGAACCT GCCGACCTG AACTGGGCG
541 ATTGAACAA GCTGAAAGTG GGCGAATGGG TCCTGGCCAT CGGTTCGCGG TTCGGCTTCC
601 ATCACTCGGT CACCGCCGGT ATCGTCAGTG CCAAGGGGCG TAGCCTGCGG AACGAGAGCT
661 ACGTACCCTT CATCCAGACC GACGTGGCGA TCAACCCGGG CAACTCCGGC GGTCCGCTGC
721 TGAACCTGGA GGGCGAAGTG GTCGGCATCA ACTCGCAGAT CTTACCCCGT TCCGGCGGCT
781 TCATGGGCCT GTCCTTCGCC ATCCCGATCG ATGTCGCGCT GAACGTCGCC GACCAGTTGA
841 AGAAAGCCGG CAAGGTCAGC CGCGGCTGGC TGGGTGTGGT GATCCAGGAA GTGAACAAGG
901 ATCTCGCCGA GTCCTTCGGC CTCGACAAGC CGTCCGGCGC GCTGGTGGCG CAGCTGGTGG
961 AAGACGGTCC GCGGCCAAG GCGGCCCTGC AGGTGGGCGA TGTGATCCTC AGCCTGAACG
1021 GCCAGTCGAT CAACGAGTCC GCCGACCTGC CGCACCTGGT GGGCAACATG AAGCCGGGCG
1081 ACAAGATCAA CCTGGACGTG ATTCGCAACG GCCAGCGCAA GTCCTTGAGC ATGGCGGTAG
1141 GCAACCTTCC GGACGACGAC GAGGAAATCG CCTCGATGGG CGCTCCGGGC GCCGAGCGCA
1201 GCAGCAACCG CCTGGGCGTG ACCGTCGCCG ACCTGACCGC CGAGCAGCGC AAGAGCCTGG
1261 ATATCCAGGG CGGCGTGGTG ATCAAGGAAG TCCAGGACGG TCCGGCCGCG GTCATCGGCC
1321 TGCGTCCGGG CGATGTCATC ACCACCTGG ACAACAAGGC GGTGACCTCG ACCAAGATCT
1381 TCGCCGACGT GGCCAAGGCC CTGCCGAAGA ACCGTTCGGT TTCGATGCGG GTACTG

```

Fig. 27

PA14 degP protein SEQ ID NO: 132

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1  MHTLKRCMAA  MVALLALSIA  MTARAE LPDF  TPLVEQASPA  VVNISTRQKL
51  PDRAMARGQL  SIPDLEGLPP  MFRDFLERTI  PQVPRNPRGQ  QREAQSLGSG
101 FIISNDGYIL  TNNHVVDAD  EILVRLSDRS  EHKAKLVGAD  PRSDVAVLKI
151 EAKNLPTLKL  GDSNKLKVG  WVLAI GSPFG  FDHSVTAGIV  SAKGRSLPNE
201 SYVPFIQTDV  AINPGNSGGP  LLNLEGEVVG  INSQIFTRSG  GFMGLSFAIP
251 IDVALNVADQ  LKKAGKVS  RGLWGVV IQEVN  KDLAESFGLD  KPSGALVAQL
301 VEDGPAAKGG  LQVGDVILSL  NGQSINESAD  LPHLVGNMKP  GDKINLDVIR
351 NGQRKSLSMA  VGNLPDDDEE  IASMGAPGAE  RSSNRLGVTV  ADLTAEQRKS
401 LDIQGGVVIK  EVQDGPAAVI  GLRPGDVITH  LDNKAVTSTK  IFADVAKALP
451 KNRSVSMRVL

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Fig. 28

PA 8830 algD SEQ ID NO:133

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1  GCGCGACAAA  CAATCGAGGT  GAATGCGATG  CGAATCAGCA  TCTTTGGTTT
51  GGGCTATGTC  GGTGCAGTAT  GTGCTGGCTG  CCTGTCGGCA  CGCGGTCATG
101 AAGTCATTGG  TGTGGATGTC  TCCAGCACCA  AGATCGACCT  GATCAACCAG
151 GGCAAGTCGC  CCATCGTCGA  ACCGGGCCTG  GAAGCGTTGT  TGCAGCAAGG
201 CCGGCAGACC  GGACGGCTGT  CGGGCACCAC  CGACTTCAAG  AAGGCTGTGC
251 TGGACTCCGA  CGTATCGTTC  ATCTGCGTCG  GCACGCCGAG  CAAGAAGAAC
301 GGCGACCTGG  ACCTGGGCTA  CATCGAGACC  GTCTGCCGCG  AGATCGGCTT
351 CGCCATCCGC  GAGAAAGTCCG  AACGCCACAC  CGTGGTGGTG  CGCAGCACCG
401 TACTGCCGGG  CACCGTCAAC  AACGTGGTGA  TCCCGCTGAT  CGAGGACTGC
451 TCGGGCAAGA  AGGCCGGGGT  CGACTTCGGC  GTCGGCACCA  ACCCCGAATT
501 CCTCCGCGAG  AGCACCGCGA  TCAAGGACTA  CGACTTCCCG  CCGATGACCG
551 TGATCGGCGA  ACTGGACAAG  CAGACCGGCG  ACCTTCTCGA  GGAAATCTAC
601 CGCGAGCTGG  ACGCGCCGAT  CATCCGCAAG  ACCGTCGAGG  TCGCCGAGAT
651 GATCAAGTAC  ACCTGCAACG  TCTGGCACGC  CGCCAAGGTC  ACCTTCGCCA
701 ACGAGATCGG  CAACATCGCC  AAGGCGGTCT  GCGTCGACGG  CCGCGAGGTG
751 ATGGACGTGA  TCTGCCAGGA  CCACAAGCTC  AACCTGTCGC  GCTACTACAT
801 GCGTCCCGGC  TTCGCCTTCG  GCGGCTCCTG  CCTGCCCAAG  GATGTACGCG
851 CCCTCACCTA  TCGCGCCAGC  CAGCTGGACG  TCGAGCACCC  GATGCTCGGT
901 TCGTTGATGC  GCAGCAACTC  CAACCAGGTG  CAGAAGGCCT  TCGATCTCAT
951 CACCAGCCAC  GACACCCGCA  AGGTCGGCCT  GCTCGGCCTG  TCGTTCAAGG
1001 CCGGCACCGA  CGATTTGCGC  GAAAGCCCGC  TGGTGGAGCT  GGCCGAGATG
1051 CTCATCGGCA  AGGGCTACGA  GTTCCGCATC  TTCGACCGCA  ACGTCGAATA
1101 CGCGCGTGTC  CACGGGGCCA  ACAAGGAATA  CATCGAGTCG  AAGATCCCGC
1151 ACGTCTCCTC  GCTGCTGGTC  TCCGACCTCG  ACGAAGTGGT  GGCGAGTTCC
1201 GATGTGCTGG  TGCTGGGCAA  TGCGACGAG  CTGTTCGTCG  ACCTGGTGAA
1251 CAAGACCCCG  AGCGGCAAGA  AGCTGGTCGA  CCTGGTGGGC  TTCATGCCCG
1301 ACACCACCAC  TGCCAGGCC  GAGGGCATCT  GCTGGTAGCG  G

```

Fig. 29

>Contig1126 of Mutant 25A12 SEQ ID NO: 135

```

..AACACCGGACGCGCCCCGATCATGTGCGCTGAGCGCTACGCTACCGTCAA
CGAAAAAGGCCACCTCGGGGTGGCCTTTTCGCGTTCTCGCACCGATCGCG
CGGAATATCGGCGGTTAACGCCTCTCCCCCGTGCGCACCTGCGGCTGAGC
CTCAGAACGAAGTCCGGCGGTAGGCACGGTAGCGCGGAACAGAAAGTTC
GCCTCGATGGCGTCGTTAGTACCTCGTCGCTGGTATGCAGGGCCTTGCC
CTCGGCCTGGGCCTGCTTGGCCACGGCGACGGCGATGCGCTTGCTGACCT
CGCGGATGTCGCCCAGCGCCGGCAACACGGCGCCCTCGCCCTGGGTAACG
ATCGGCGAGCAGTTGGCCAGGGCGTTGGCCGCGGCCATCAGCATGCCTTC
GGTGACCCGATTGGCCCCGCGGGCGATCACCCCGAGCCGATGCCGGGGA
AGATATAGGCGTTGTTGCACTGGGCGATGGGAATCCGCTTGTCGCCACC
TGCACCGGTTGGAACGGGCTACCGGTGGCGACCAGCGCCTGGCCGTCGGT
CCAGTTGAGGATTTCTGCGGAGTCGCCTCGACCCGCGAGGTCGGGTTGG
ACAGCGGCATCACCAGCGGCTGCTTGCAATGGCTGTGCAGCTCACGGATG
ACCTCTTCGGAAAAACAGCCCGCGCTGCCCGGAGACGCCGATCAGCACCGT
CGGCCGGGCATTGCGGATCACTTCCAGCAACGCCAGGTCGTCGCCCTGCT
GGCCGCCCCAGGCACCGAGATCGGCGCGCTTCTGCGCCAGGCGGTGCTGG
AAGTCGACCAGGTTGCTCATGTCGTCGGTGAGCAGGCCCCAGCGGTCGAC
CATGAAGATGCGCCGACGCGCCTGGGCCTCGTCCAGGCCCTCCAGTTGCA
TGGCGGCGATGATCTGTTTCGGCGATGCCGCAACCGGCGGAGGGGCGCCGA
CGAAGGTACGGTCTGCTCGCTGAGCTTCTCGCCCTTGGCCTTGCAAGCC
GCCAGCAGGGTGCCACGGCCACCGCGGCGGTGCCCTGGATGTCGTCGTT
GAAGCAGCACAGCTCGTCCTTGTAAGCGCTCCAGCAACGGCATGGCATTGG
TCTGGGCGAAGTCTTGAATTGCAGCAGGACGTTGGGCCAGCGGCGCTTG
ATCGCCTGGATGAACAGGTGACGAACTCCTCGTACTGCGCCCCGCTCAC
CCGCTCGTGGCGCCACCAATGTACATCGGGTCGTTGAGCAGGTCCGGGT
TGTTGGTGCCGACGTCCAGCACCACCGGCAGGGTGTAGGCCGGGCTGATA
CCGCCGAGGTGTAACAGGGGACAGCTTGCCGATCGGGATGCCCATCCGG
CCGATGCCCTGGTTGCCGAGGGCGAGGATCGGCTGGCTGTCGGTACAAAA
CAATCTAAGGTGTCTTTGGTGGCTGAAGGAGTTTCAATCGTTCGGGCCG
GGAAGAATAAAGGCCCGGTGGGTCGAACTTTGAATCTGGAAGGTTGCAA
ACTGGGGGAAAAAATGGAATTTTTTAAGAGCCTAAGAGCGGAAAAAAGTT
CTTTTTCTAAAAAGAAAAAATGGGGAAAAAGTTGAAAAGTATATGATAA
GAGCAGGTGTCAAAATGAATGTTTTGAAAGCCAGTGAAATAAACTCTGG
AAAAGGCAGTTATAAGGGCTATAAAAGGGATGAAAAAGAAGTGTGTGAA
ATAACGAAAGGCAATAGGGAAAA

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Fig. 31

ORF A (610>1371)
ORF B (161>961)
ORF C (937>1449)

33C7 contig Map (1 > 2048) ORF Map

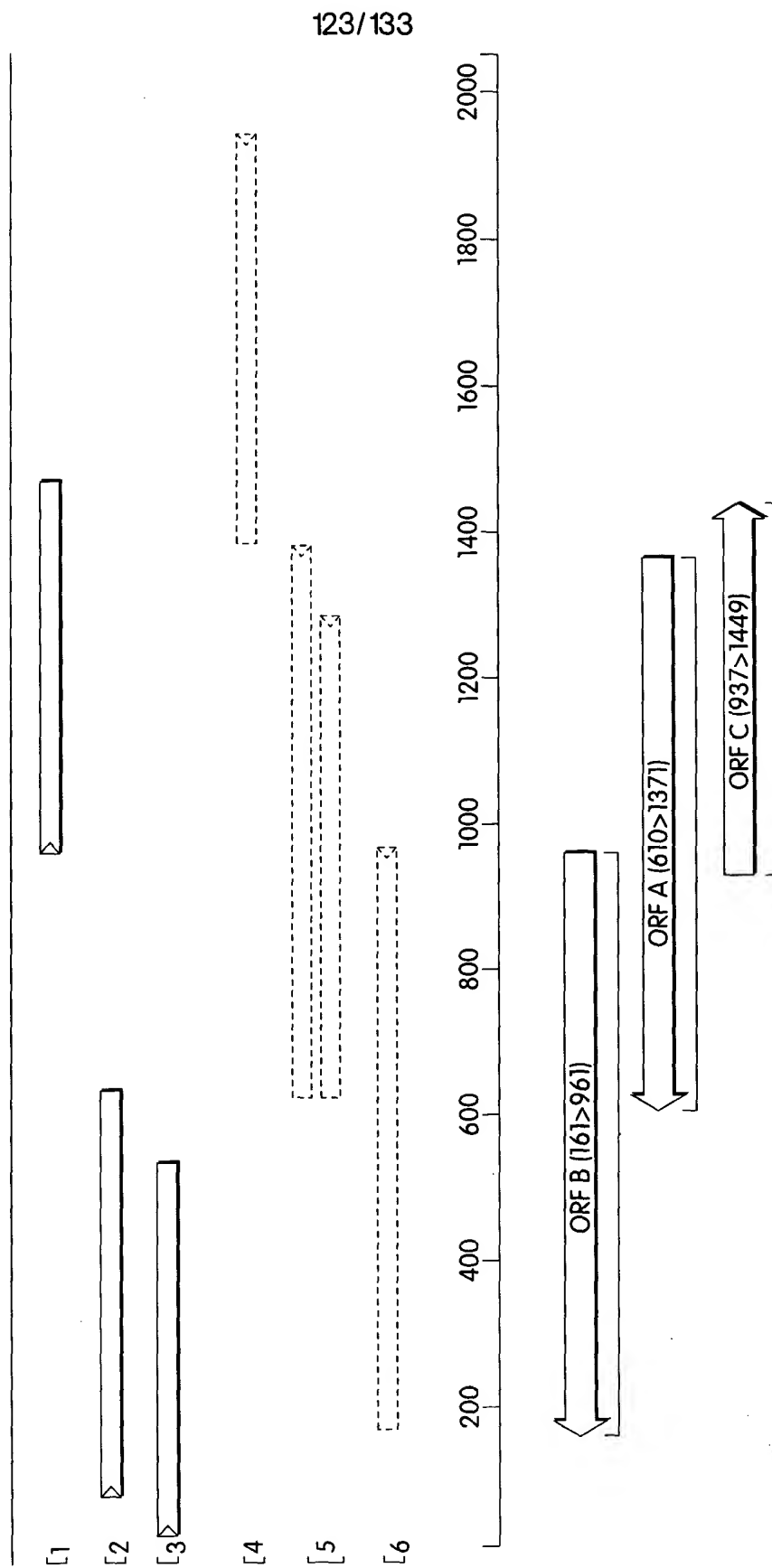


Fig. 32A

124/133

Sequence: 33C7 contig From: 1 To: 2048

10	20	30	40	50	60
AGCTTATGCA	TGCGGCCGCA	TCTAGAGGGC	CCGGATCCGG	TGACCATCGG	TCACCGGCAT 60
GCCGGTGGTT	TCGGTATCCA	GTACGACGCT	ACGCATCTAT	AGAGCCTTTC	TCTGTTTCGC 120
TGCAGCCGTG	GCTGCTGAAC	GCTTGTTTCG	GTGTGGCCGC	TCAGCGCGGC	AATTCGGCGA 180
CGCCACGGTT	GGCCAACTGG	TCGGCCCCGT	CGTTGCCGGG	GTCGCCGGTA	TGCCCCGCGA 240
CCCACTGCCA	CTCCACCTGG	TGCCGGGCGA	CCTGTTCATC	CAGGGCCTGC	CAGAGGTCGG 300
310	320	330	340	350	360
CATTCTTGAC	AGGCTGCTTG	CTGGCGGTCT	TCCAGCCGCG	CTTCTTCCAG	TTCGGCAACC 360
ATTCGGTGAT	GCCGCGCATC	ACGTATTCCG	AGTCGGTGAT	CAGACGGATC	GGACAGGAAC 420
GCTTGAGTGC	CGCCAGCGCC	TGGATCGCCG	CCATCAGCTC	CATGCGGTTG	TTGGTGGTGT 480
CCGGCTCGCC	GCCCCAAAGC	TCTCGCTCGG	CGCCCTTGTA	GAGGAGCAAC	GCCCCCAGC 540
CGCCGCGCCC	AGGGTTGCCC	TTGCAGGCGC	CGTCGGTATA	GATCACTACC	TGTTCTTTAT 600
610	620	630	640	650	660
CTGTCA TGCC	TAAATTTCCG	AATCTCGCCG	GCTGACTTTC	GCCACCGGCA	TGGGCACCAG 660
CTGACCGCGC	GGTTCGCGCT	TGCTCTGGCG	CAACGGGCGC	AACCCACGA	CCAGCTTGCG 720
TGCCACCAAT	AGATAGAAGC	CGGCGCCCGA	AGACTGCCAG	GCGTCGCCCC	AGCGCTCCAG 780
GCGAGCCAGG	CGCGATTGCC	AGGCTGCCGA	CGCAAGCGGC	GGACGATAGC	ACCCGAAGCG 840
CCGTTTCTCC	AGCGCGAAGC	CCAGCAGGTT	GAGCCAATCG	CAGGCCCGCG	ACGGAGGAAT 900
910	920	930	940	950	960
GCAGCGGGCC	TGGCGCAAGG	CATCCCCGGC	GAAATAATGA	CGGATGCCCC	ACAGGCTCCA 960
TGGGTTGATG	CCGATCAGCA	GCAGGTGGCC	GCCCCGACGA	ACGGTACGCG	CGGCTTCGCG 1020
CAGGAGACGG	TGAGGCGACA	GGCAGAAATC	CAGGCCGTGT	TGCAGCAGGA	CCACGTCCGC 1080
GGCATGTTTC	CTGAGCGGCC	AGGCGCCCTC	TTCGCAGGCG	ATGTCCACGC	CCGGCAGCGG 1140
CGGCCCCAGG	CGCACGCCGC	GCTGAATCTG	CCCGGTGCTC	GGCGGCAGTT	CGGCATGCGG 1200
1210	1220	1230	1240	1250	1260
CCCGTAGTGC	ACCAGGTAGC	CACCGAAGTA	ACGGGTCAGC	TCGTGCACAC	ACAGGCGTCG 1260
CTCCTCGGCC	AGCATCAGGC	TGCCCAGCGG	GCCCTGGAAC	CAGTCGCGCG	CCCGGTTGAT 1320
CGATGCCAGC	CACTCGGCAT	CGGTCTGGGC	GAAGGCTTGC	GGTTCGTTCA	TGCGTACCTC 1380
CAGCGTCTTC	CCCTTCGCGG	CGACGGACGC	CGGCACGACG	GGAAAATAAG	CAATACTATG 1440
CGCCAATGAC	TTCTGCTTAG	CGACATCGAC	CCATGATACA	GATCGACGCC	CTGCCCGCCT 1500

Fig. 32B

Sequence: 33C7 contig From: 1 To: 2048 (continued)

126/133

Sequence: 33C7 ORF A From: 1 To: 254

```

      10      20      30      40
      |      |      |      |
MNEPQAFQQT DAEWLASINR ARDWFQGPLG SLMLAEERRL 40
LCDELTRYFG GYLVHYGPHA ELPPSTGQIQ RGVRLGPPLP 80
GVDIACEEGA WPLSEHAADV VLLQHGLDFC LSPHRLRLREA 120
ARTVRPGGHL LLIGINPWSL WGIRHYFAGD ALRQARCIPP 160
SRACDWLNLL GFALEKRRFG CYRPPLASAA WQSRLARLER 200

WGDAWQSSGA GFYLLVARKL VVGLRPLRQS KREPRGQLVP 240
MPVAKVSRRD SEI. 254

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Fig. 32E

Sequence: 33C7 ORF B From: 1 To: 801

```

      10      20      30      40      50      60
      |      |      |      |      |      |
ATGGAGCCTG TGGGGCATCC GTCATTATTT CGCCGGGGAT GCCTTGCGCC AGGCCCGCTG 60
CATTCTCTCC TCGCGGGCCT GCGATTGGCT CAACCTGCTG GGCTTCGCGC TGGAGAAACG 120
GCGCTTCGGG TGCTATCGTC CGCCGCTTGC GTCGGCAGCC TGGCAATCGC GCCTGGCTCG 180
CCTGGAGCGC TGGGGCGACG CCTGGCAGTC TTCGGGCGCC GGCTTCTATC TATTGGTGGC 240
ACGCAAGCTG GTCGTGGGGT TGCGCCCGTT GCGCCAGAGC AAGCGCGAAC CGCGCGGTCA 300
      310      320      330      340      350      360
      |      |      |      |      |      |
GCTGGTGCCC ATGCCGGTGG CGAAAGTCAG CCGGCGAGAT TCCGAAATTT AGGCATGACA 360
GATAAAGAAC AGGTAGTGAT CTATACCGAC GGCGCCTGCA AGGGCAACCC TGGGCGCGGC 420
GGCTGGGGGG CGTTGCTCCT CTACAAGGGC GCCGAGCGAG AGCTTGGGG CGGCGAGCCG 480
GACACCACCA ACAACCGCAT GGAGCTGATG GCGGCGATCC AGGCGCTGGC GGCACCTAAG 540
CGTTCTCTGT CGATCCGTCT GATACCGAC TCGGAATACG TGATGCGCGG CATCACCAG 600
      610      620      630      640      650      660
      |      |      |      |      |      |
TGGTTGCCGA ACTGGAAGAA GCGCGGCTGG AAGACCGCCA GCAAGCAGCC TGTCAGAAT 660
GCCGACCTCT GGCAGGCCCT GGATGAACAG GTCGCCCCGC ACCAGGTGGA GTGGCAGTGG 720
GTCCGCGGGC ATACCGGCGA CCCCAGCAAC GAGCGGGCCG ACCAGTTGGC CAACCGTGGC 780
GTCGCCGAAT TGCCGCGCTG A 801

```

Fig. 32F

Sequence: 33C7 ORF B PROTEIN From: 1 To: 267

```

      10      20      30      40      50
      |      |      |      |      |
MEPVGHPSLF RRGCLAPGPL HSSVAGLRLA QPAGLRAGET ALRVLSSAAC 50
VGSIAIAPGS PGALGRRLLAV FGRRLLSIGG TQAGRGVAPV APEQARTARS 100
AGAHAGGESQ PARFRNLGMT DKEQVVIYTD GACKGNPGRG GWGALLLYKG 150
AERELWGGEF DTTNNRMELM AAIQALAALK RSCPIRLITD SEYVMRGITE 200
WLPNWKRGW KTASKQPVKN ADLWQALDEQ VARHQVEWQW VRGHTGDPGN 250
      260      270      280      290      300
      |      |      |      |      |
ERADQLANRG VAE LPR. 267

```

Fig. 32G

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33C7 ORF C

	10	20	30	40	50	60	
ATGACGGATG	CCCCACAGGC	TCCATGGGTT	GATGCCGATC	AGCAGCAGGT	GGCCGCCCCG	60	
ACGAACGGTA	CGCGCGGCTT	CGCGCAGGAG	ACGGTGAGGC	GACAGGCAGA	AATCCAGGCC	120	
GTGTTGCAGC	AGGACCACGT	CCGCGGCATG	TTCGCTGAGC	GGCCAGGCGC	CCTCTTCGCA	180	
GGCGATGTCC	ACGCCCCGCA	GCGGCGGCC	CAGGCGCACG	CCGCGCTGAA	TCTGCCCCGT	240	
GCTCGGCGGC	AGTTCGGCAT	GCGGCCCGTA	GTGCACCAGG	TAGCCACCGA	AGTAACGGGT	300	
	310	320	330	340	350	360	
CAGCTCGTCG	CACAACAGGC	GTCGCTCCTC	GGCCAGCATC	AGGCTGCCCA	GCGGGCCCTG	360	
GAACCACTCG	CGCGCCCGGT	TGATCGATGC	CAGCCACTCG	GCATCGGTCT	GGGCGAAGGC	420	
TTGCGGTTCG	TTCATGCGTA	CCTCCAGCGT	CTTCCCCTTC	GCGGCGACGG	ACGCCGGCAC	480	
GACGGGAAAA	TAAGCAATAC	TATGCGCCAA	TGA	513			

Fig. 32H

Sequence: 33C7 ORF C PROTEIN From: 1 To: 171

	10	20	30	40	50	
MTDAPQAPWV	DADQQQVAAR	TNGTRGFAQE	TVRRQAEIQA	VLQQDHVRGM	50	
FAERPGALFA	GDVHARQRRP	QAHAALNLPG	ARRQFGMRPV	VHQVATEVTG	100	
QLVAQQASLL	GQHQAQRAL	EPVARPVDR	QPLGIGLGEG	LRFVHAYLQR	150	
LPLRGDGRRH	DGKISNTMRQ	.	171			

Fig. 32I

1	NTTGTGTTAA	GATCAGGCTT	GGTGGTGAAG	AAAGGTTCGA	ACNNGTGGTC
51	AATGATCNAC	TTCGGGGATN	CNGCTGCCCC	TATNATTCAA	CACGTGGTCA
101	AACGGTATGT	TCCGAGGCGT	CTGNCCACCN	GTACTAGTCG	ACGC

Fig. 33

1940-41	1941-42	1942-43	1943-44	1944-45	1945-46	1946-47	1947-48	1948-49	1949-50	1950-51	1951-52	1952-53	1953-54	1954-55	1955-56	1956-57	1957-58	1958-59	1959-60	1960-61	1961-62	1962-63	1963-64	1964-65	1965-66	1966-67	1967-68	1968-69	1969-70	1970-71	1971-72	1972-73	1973-74	1974-75	1975-76	1976-77	1977-78	1978-79	1979-80	1980-81	1981-82	1982-83	1983-84	1984-85	1985-86	1986-87	1987-88	1988-89	1989-90	1990-91	1991-92	1992-93	1993-94	1994-95	1995-96	1996-97	1997-98	1998-99	1999-00	2000-01	2001-02	2002-03	2003-04	2004-05	2005-06	2006-07	2007-08	2008-09	2009-10	2010-11	2011-12	2012-13	2013-14	2014-15	2015-16	2016-17	2017-18	2018-19	2019-20	2020-21	2021-22	2022-23	2023-24	2024-25	2025-26	2026-27	2027-28	2028-29	2029-30	2030-31	2031-32	2032-33	2033-34	2034-35	2035-36	2036-37	2037-38	2038-39	2039-40	2040-41	2041-42	2042-43	2043-44	2044-45	2045-46	2046-47	2047-48	2048-49	2049-50	2050-51	2051-52	2052-53	2053-54	2054-55	2055-56	2056-57	2057-58	2058-59	2059-60	2060-61	2061-62	2062-63	2063-64	2064-65	2065-66	2066-67	2067-68	2068-69	2069-70	2070-71	2071-72	2072-73	2073-74	2074-75	2075-76	2076-77	2077-78	2078-79	2079-80	2080-81	2081-82	2082-83	2083-84	2084-85	2085-86	2086-87	2087-88	2088-89	2089-90	2090-91	2091-92	2092-93	2093-94	2094-95	2095-96	2096-97	2097-98	2098-99	2099-00	2100-01	2101-02	2102-03	2103-04	2104-05	2105-06	2106-07	2107-08	2108-09	2109-10	2110-11	2111-12	2112-13	2113-14	2114-15	2115-16	2116-17	2117-18	2118-19	2119-20	2120-21	2121-22	2122-23	2123-24	2124-25	2125-26	2126-27	2127-28	2128-29	2129-30	2130-31	2131-32	2132-33	2133-34	2134-35	2135-36	2136-37	2137-38	2138-39	2139-40	2140-41	2141-42	2142-43	2143-44	2144-45	2145-46	2146-47	2147-48	2148-49	2149-50	2150-51	2151-52	2152-53	2153-54	2154-55	2155-56	2156-57	2157-58	2158-59	2159-60	2160-61	2161-62	2162-63	2163-64	2164-65	2165-66	2166-67	2167-68	2168-69	2169-70	2170-71	2171-72	2172-73	2173-74	2174-75	2175-76	2176-77	2177-78	2178-79	2179-80	2180-81	2181-82	2182-83	2183-84	2184-85	2185-86	2186-87	2187-88	2188-89	2189-90	2190-91	2191-92	2192-93	2193-94	2194-95	2195-96	2196-97	2197-98	2198-99	2199-00	2200-01	2201-02	2202-03	2203-04	2204-05	2205-06	2206-07	2207-08	2208-09	2209-10	2210-11	2211-12	2212-13	2213-14	2214-15	2215-16	2216-17	2217-18	2218-19	2219-20	2220-21	2221-22	2222-23	2223-24	2224-25	2225-26	2226-27	2227-28	2228-29	2229-30	2230-31	2231-32	2232-33	2233-34	2234-35	2235-36	2236-37	2237-38	2238-39	2239-40	2240-41	2241-42	2242-43	2243-44	2244-45	2245-46	2246-47	2247-48	2248-49	2249-50	2250-51	2251-52	2252-53	2253-54	225
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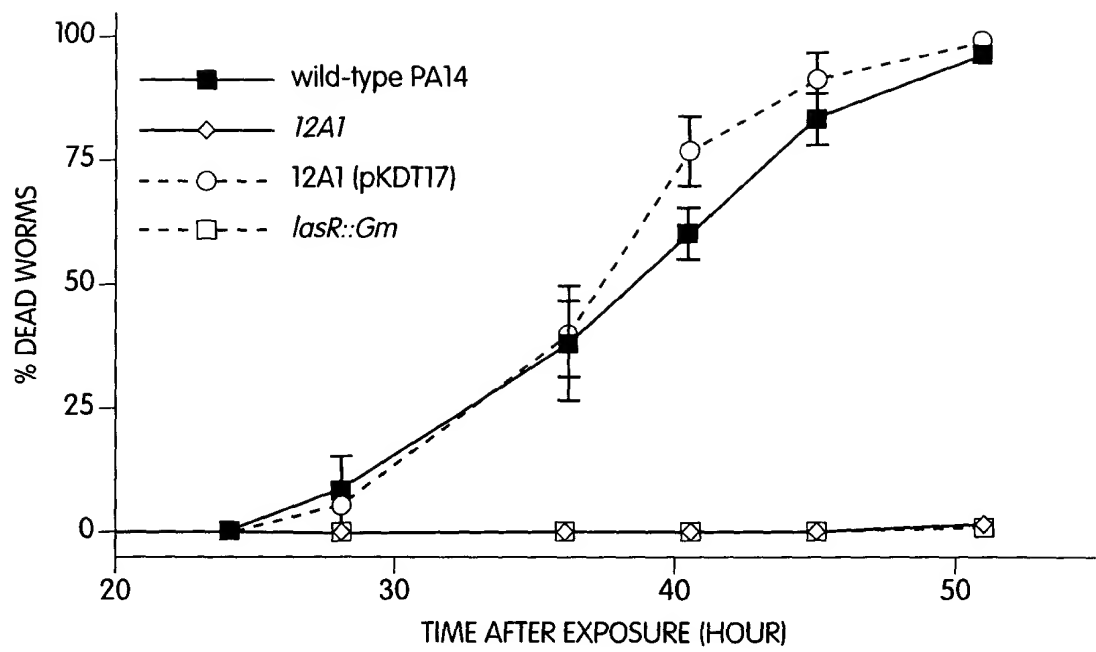


Fig. 34A

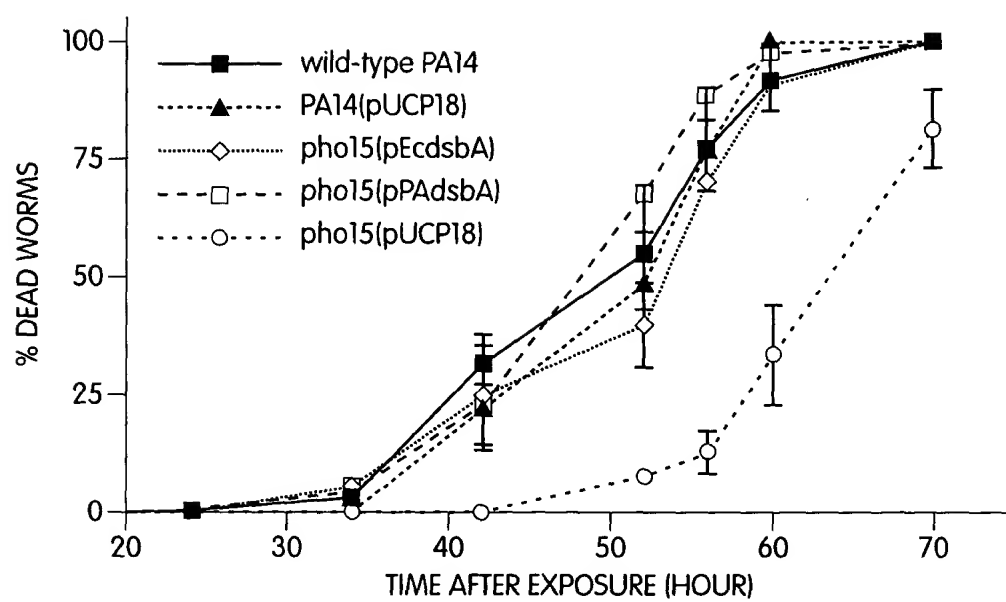


Fig. 34B

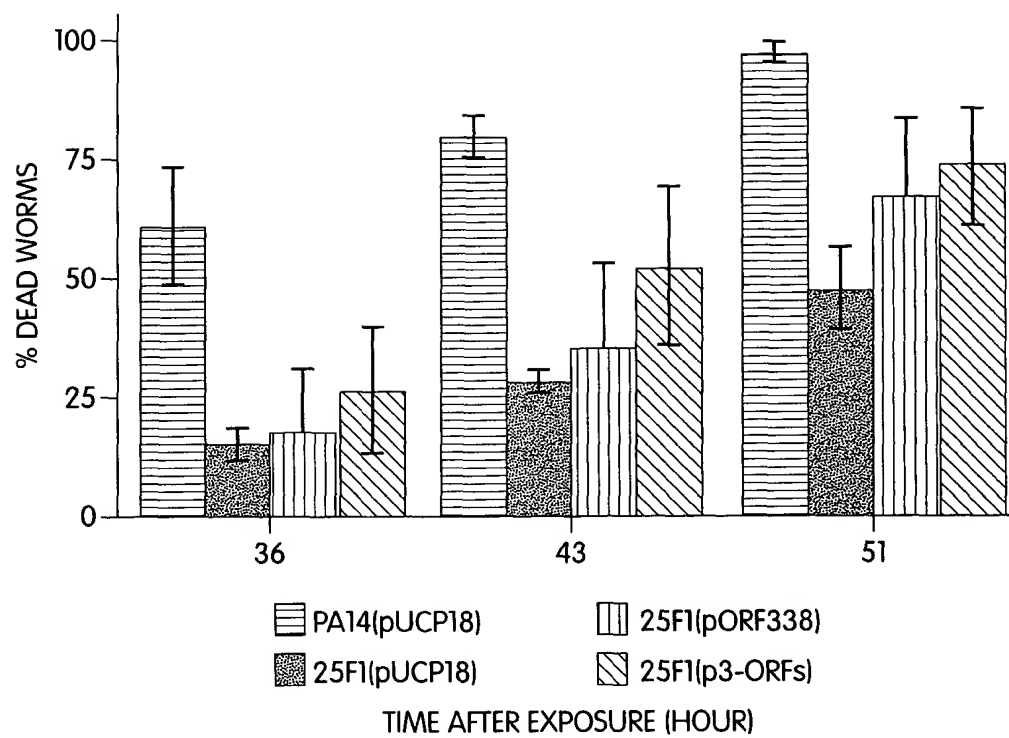


Fig. 34C

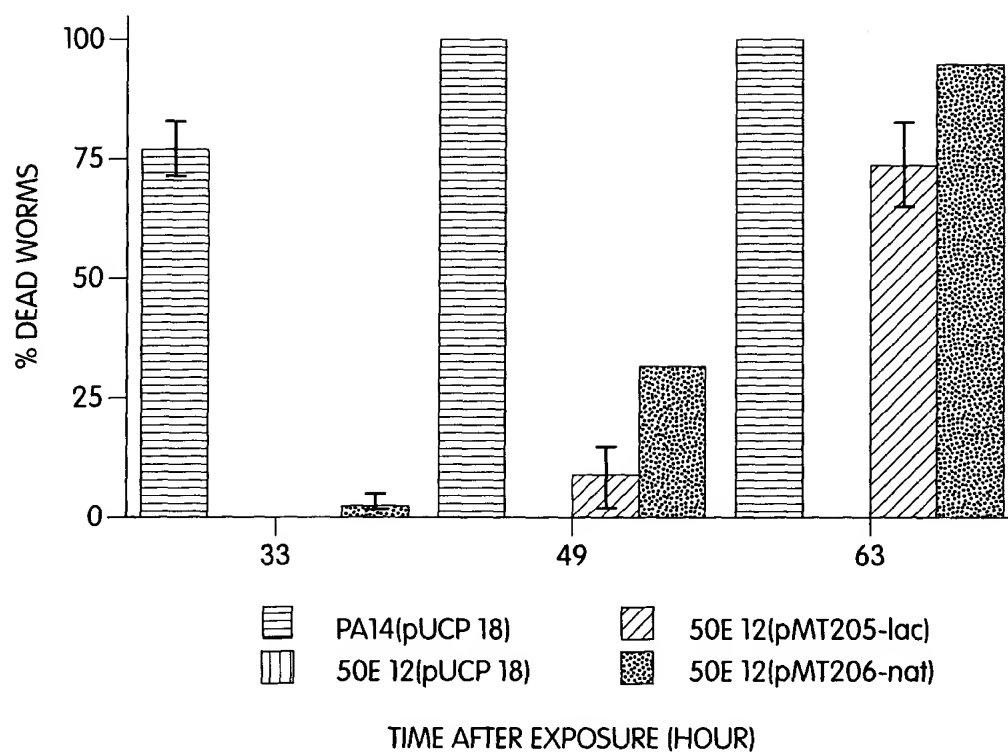


Fig. 34D

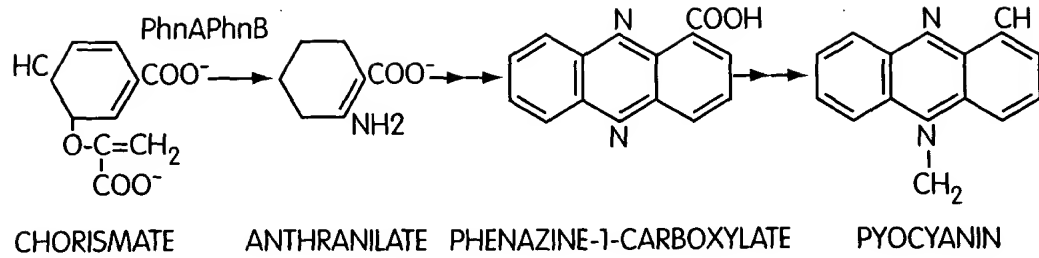


Fig. 35A

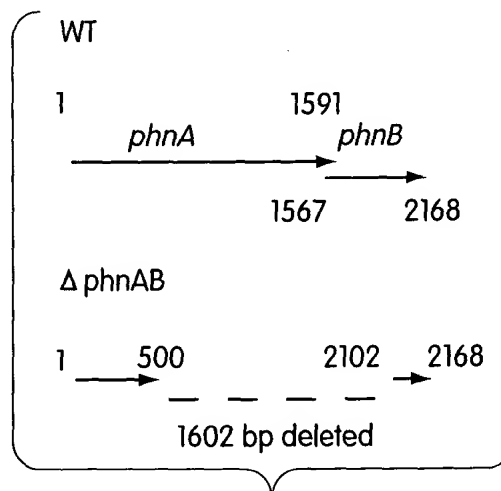


Fig. 35B

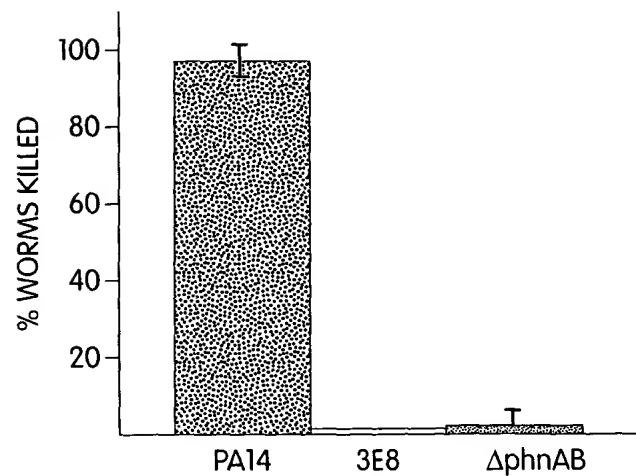


Fig. 35C